GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 12:19:49 ; Search time 1699 Seconds
(without alignments)
669.140 Million cell updates/sec

Title: US-10-605-498-82
Perfect score: 20
Sequence: 1 gggacgcggcgctcggtcat 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 2097806

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
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8: gb_pr:*
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10: gb_sts:*
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12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	20	100.0	20	6	CQ799984	CQ799984 Sequence
	2	20	100.0	21	6	CQ799983	CQ799983 Sequence
c	3	19	95.0	19	6	CQ799992	CQ799992 Sequence
	4	16	80.0	21	6	CQ799905	CQ799905 Sequence
	5	15	75.0	21	6	CQ799906	CQ799906 Sequence
	6	14.2	71.0	33	6	AR559501	AR559501 Sequence
	7	14.2	71.0	33	6	AX473165	AX473165 Sequence
	8	13.8	69.0	42	6	AR041097	AR041097 Sequence
	9	13.8	69.0	42	6	AR060705	AR060705 Sequence
	10	13.8	69.0	42	6	AR063138	AR063138 Sequence
	11	13.8	69.0	42	6	AR117027	AR117027 Sequence
	12	13.8	69.0	42	6	I64789	I64789 Sequence 14
	13	13.2	66.0	27	6	E41696	E41696 Process for
	14	13.2	66.0	43	6	AX496977	AX496977 Sequence
	15	13.2	66.0	43	6	AX703486	AX703486 Sequence
	16	13.2	66.0	43	6	AX720926	AX720926 Sequence
	17	13.2	66.0	43	6	AX925315	AX925315 Sequence
	18	13.2	66.0	43	6	AX925574	AX925574 Sequence
	19	13	65.0	20	6	AR454276	AR454276 Sequence
c	20	12.8	64.0	23	6	BD243529	BD243529 Nucleotid
c	21	12.8	64.0	23	6	AX034952	AX034952 Sequence
	22	12.8	64.0	24	6	AX684030	AX684030 Sequence
c	23	12.8	64.0	37	6	AR379389	AR379389 Sequence
	24	12.8	64.0	40	6	AR053662	AR053662 Sequence
c	25	12.8	64.0	40	6	AR053704	AR053704 Sequence
	26	12.8	64.0	40	6	AR258597	AR258597 Sequence
c	27	12.8	64.0	40	6	AR258639	AR258639 Sequence
c	28	12.6	63.0	24	6	BD081436	BD081436 Productio
c	29	12.6	63.0	24	6	AR429358	AR429358 Sequence
c	30	12.6	63.0	24	6	AR579704	AR579704 Sequence
c	31	12.6	63.0	24	6	AR628409	AR628409 Sequence
c	32	12.6	63.0	30	6	AR229807	AR229807 Sequence
	33	12.6	63.0	30	6	AR363940	AR363940 Sequence
	34	12.6	63.0	37	6	A07707	A07707 Oligonucleo
	35	12.6	63.0	37	6	A10006	A10006 Nucleotide
c	36	12.6	63.0	39	6	AR092584	AR092584 Sequence
c	37	12.6	63.0	39	6	BD076530	BD076530 Fibroblas
	38	12.6	63.0	42	6	BD141508	BD141508 Method fo
	39	12.6	63.0	42	6	BD176004	BD176004 Method fo
c	40	12.6	63.0	50	6	CQ006708	CQ006708 Sequence
c	41	12.6	63.0	50	6	AX960340	AX960340 Sequence
	42	12.6	63.0	50	6	AX960395	AX960395 Sequence
	43	12.4	62.0	20	6	AR014592	AR014592 Sequence
	44	12.4	62.0	20	6	I26721	I26721 Sequence 9
	45	12.4	62.0	20	6	AR235394	AR235394 Sequence

ALIGNMENTS

RESULT 1
CQ799984
LOCUS CQ799984 20 bp DNA linear PAT 28-APR-2004
DEFINITION Sequence 82 from Patent WO2004030660.
ACCESSION CQ799984
VERSION CQ799984.1 GI:46848931
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Gleave,M.E., Rocchi,P. and Signaevsky,M.
TITLE Compositions for treatment of prostate and other cancers
JOURNAL Patent: WO 2004030660-A 82 15-APR-2004;
The University of British Columbia (CA)
FEATURES Location/Qualifiers
source 1. .20
/organism="Homo sapiens"
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGCGGCGCTCGGTCAT 20
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Db 1 GGGACGCGGCGCTCGGTCAT 20

RESULT 2
CQ799983
LOCUS CQ799983 21 bp DNA linear PAT 28-APR-2004
DEFINITION Sequence 81 from Patent WO2004030660.
ACCESSION CQ799983
VERSION CQ799983.1 GI:46848930
KEYWORDS .
SOURCE Homo sapiens (human)

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  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gleave,M.E., Rocchi,P. and Signaevsky,M.
  TITLE     Compositions for treatment of prostate and other cancers
  JOURNAL   Patent: WO 2004030660-A 81 15-APR-2004;
            The University of British Columbia (CA)
FEATURES             Location/Qualifiers
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Qy          1 GGGACGCGGCGCTCGGTCAT 20
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Db          2 GGGACGCGGCGCTCGGTCAT 21


RESULT 3
CQ799992/c
LOCUS       CQ799992                 19 bp    RNA     linear   PAT 28-APR-2004
DEFINITION  Sequence 90 from Patent WO2004030660.
ACCESSION   CQ799992
VERSION     CQ799992.1  GI:46848939
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gleave,M.E., Rocchi,P. and Signaevsky,M.
  TITLE     Compositions for treatment of prostate and other cancers
  JOURNAL   Patent: WO 2004030660-A 90 15-APR-2004;
            The University of British Columbia (CA)
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
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Qy          2 GGACGCGGCGCTCGGTCAT 20
              ||||||||||||||||||||
Db         19 GGACGCGGCGCTCGGTCAT 1


RESULT 4
CQ799905
LOCUS       CQ799905                 21 bp    DNA     linear   PAT 28-APR-2004
DEFINITION  Sequence 3 from Patent WO2004030660.
ACCESSION   CQ799905
VERSION     CQ799905.1  GI:46848852
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gleave,M.E., Rocchi,P. and Signaevsky,M.
  TITLE     Compositions for treatment of prostate and other cancers
  JOURNAL   Patent: WO 2004030660-A 3 15-APR-2004;
            The University of British Columbia (CA)
FEATURES             Location/Qualifiers
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Qy          5 CGCGGCGCTCGGTCAT 20
              ||||||||||||||||
Db          1 CGCGGCGCTCGGTCAT 16


RESULT 5
CQ799906
LOCUS       CQ799906                 21 bp    DNA     linear   PAT 28-APR-2004
DEFINITION  Sequence 4 from Patent WO2004030660.
ACCESSION   CQ799906
VERSION     CQ799906.1  GI:46848853
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gleave,M.E., Rocchi,P. and Signaevsky,M.
  TITLE     Compositions for treatment of prostate and other cancers
  JOURNAL   Patent: WO 2004030660-A 4 15-APR-2004;
            The University of British Columbia (CA)
FEATURES             Location/Qualifiers
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Qy          1 GGGACGCGGCGCTCG 15
              |||||||||||||||
Db          7 GGGACGCGGCGCTCG 21


RESULT 6
AR559501
LOCUS       AR559501                 33 bp    DNA     linear   PAT 08-OCT-2004
DEFINITION  Sequence 16 from patent US 6750042.
ACCESSION   AR559501
VERSION     AR559501.1  GI:53968947
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Summers,A.O. and Caguiat,J.J.
  TITLE     Metal binding proteins, recombinant host cells and methods
  JOURNAL   Patent: US 6750042-A 16 15-JUN-2004;
            University of Georgia Research Foundation, Inc.; Athens, GA
FEATURES             Location/Qualifiers
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ORIGIN

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Qy          1 GGGACGCGGCGCTCGGTCA 19
              ||| | |||||||||| ||
Db          6 GGGTCTCGGCGCTCGGGCA 24


RESULT 7
AX473165
LOCUS       AX473165                 33 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 16 from Patent WO0230962.
ACCESSION   AX473165
VERSION     AX473165.1  GI:22207875
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Summers,A.O. and Caguiat,J.J.
  TITLE     Metal binding proteins, recombinant host cells and methods
  JOURNAL   Patent: WO 0230962-A 16 18-APR-2002;
            UNIVERSITY OF GEORGIA RESEARCH FOUNDATION, INC. (US)
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="primer"
ORIGIN

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  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GGGACGCGGCGCTCGGTCA 19
              ||| | |||||||||| ||
Db          6 GGGTCTCGGCGCTCGGGCA 24


RESULT 8
AR041097
LOCUS       AR041097                 42 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 21 from patent US 5811264.
ACCESSION   AR041097
VERSION     AR041097.1  GI:5961593
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 42)
  AUTHORS   Aitken,J.F., Apostol,I.Z., Lippincott,J.A. and Levine,J.D.
  TITLE     Proteins with mutations to decrease N-terminal methylation
  JOURNAL   Patent: US 5811264-A 21 22-SEP-1998;
FEATURES             Location/Qualifiers
     source          1. .42
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                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             69.0%;  Score 13.8;  DB 6;  Length 42;
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  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 ACGCGGCGCTCGGTCAT 20
              |||| |||||||||| |
Db         16 ACGCTGCGCTCGGTCGT 32


RESULT 9
AR060705
LOCUS       AR060705                 42 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 14 from patent US 5840851.
ACCESSION   AR060705
VERSION     AR060705.1  GI:5987155
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 42)
  AUTHORS   Plomer,J.Jeffrey., Ryland,J.R., Matthews,M.-A.H., Traylor,D.W.,
            Milne,E.E., Durfee,S.L., Mathews,A.J. and Neway,J.O.
  TITLE     Purification of hemoglobin
  JOURNAL   Patent: US 5840851-A 14 24-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .42
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

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  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 ACGCGGCGCTCGGTCAT 20
              |||| |||||||||| |
Db         16 ACGCTGCGCTCGGTCGT 32


RESULT 10
AR063138
LOCUS       AR063138                 42 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 17 from patent US 5844090.
ACCESSION   AR063138
VERSION     AR063138.1  GI:5990829
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 42)
  AUTHORS   Anderson,D.C., Mathews,A.J., Trimble,S.P. and Anthony-Cahill,S.
  TITLE     Modified hemoglobin-like compounds
  JOURNAL   Patent: US 5844090-A 17 01-DEC-1998;
FEATURES             Location/Qualifiers
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  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 ACGCGGCGCTCGGTCAT 20
              |||| |||||||||| |
Db         16 ACGCTGCGCTCGGTCGT 32


RESULT 11
AR117027
LOCUS       AR117027                 42 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 21 from patent US 6140071.
ACCESSION   AR117027
VERSION     AR117027.1  GI:14097933
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 42)
  AUTHORS   Aitken,J.F., Apostol,I.Z., Lippincott,J.A. and Levine,J.D.
  TITLE     Proteins with mutations to decrease N-terminal methylation
  JOURNAL   Patent: US 6140071-A 21 31-OCT-2000;
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
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ORIGIN

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  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 ACGCGGCGCTCGGTCAT 20
              |||| |||||||||| |
Db         16 ACGCTGCGCTCGGTCGT 32


RESULT 12
I64789
LOCUS       I64789                    42 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 14 from patent US 5665869.
ACCESSION   I64789
VERSION     I64789.1  GI:2481683
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 42)
  AUTHORS   Ryland,J.R., Matthews,M.-A.H., Ernst,U.P., Houk,D.E., Traylor,D.W.
            and Williams,L.R.
  TITLE     Method for the rapid removal of protoporphyrin from protoporphyrin
            IX-containing solutions of hemoglobin
  JOURNAL   Patent: US 5665869-A 14 09-SEP-1997;
FEATURES             Location/Qualifiers
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ORIGIN

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Qy          4 ACGCGGCGCTCGGTCAT 20
              |||| |||||||||| |
Db         16 ACGCTGCGCTCGGTCGT 32


RESULT 13
E41696
LOCUS       E41696                    27 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Process for producing L-glutamic acid by fermentaion.
ACCESSION   E41696
VERSION     E41696.1  GI:18633367
KEYWORDS    JP 2001069979-A/13.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Fujii,M. and Imanaka,T.
  TITLE     Process for producing L-glutamic acid by fermentaion
  JOURNAL   Patent: JP 2001069979-A 13 21-MAR-2001;
            JAPAN TOBACCO INC,TAKDAYUKI IMANAKA
COMMENT     OS   Artificial Sequence
            PN   JP 2001069979-A/13
            PD   21-MAR-2001
            PF   31-AUG-1999 JP 1999245121
            PR
            PI   MIKIO FUJII,TADAYUKI IMANAKA
            PC   C12N15/09,C12N1/21,C12P13/14//(C12N1/21,C12R1:15),(C12P13/14,
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ORIGIN

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Qy          3 GACGCGGCGCTCGGTCAT 20
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Db          9 GACGCGGCGAACGGCCAT 26


RESULT 14
AX496977
LOCUS       AX496977                  43 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 48 from Patent WO0222826.
ACCESSION   AX496977
VERSION     AX496977.1  GI:23342420
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Li,M., Melander,C. and Liu,H.
  TITLE     Methods and compositions for the construction and use of fusion
            libraries
  JOURNAL   Patent: WO 0222826-A 48 21-MAR-2002;
            Xencor, Inc. (US)
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Qy          1 GGGACGCGGCGCTCGGTC 18
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Db          8 GGGGCTCGGCGCTCGCTC 25


RESULT 15
AX703486
LOCUS       AX703486                  43 bp    DNA     linear   PAT 03-APR-2003
DEFINITION  Sequence 48 from Patent WO02066653.
ACCESSION   AX703486
VERSION     AX703486.1  GI:29538451
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Li,M. and Liu,Y.C.
  TITLE     Procaryotic libraries and uses
  JOURNAL   Patent: WO 02066653-A 48 29-AUG-2002;
            Xencor (US)
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Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Search completed: December 13, 2005, 13:58:20
Job time : 1701 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 08:34:39 ; Search time 260 Seconds
(without alignments)
512.669 Million cell updates/sec

Title: US-10-605-498-82
Perfect score: 20
Sequence: 1 gggacgcggcgctcggtcat 20

Scoring table: IDENTITY_NUC
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Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 4879314

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9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	20	100.0	20	12	ADM94732	Adm94732 Human hea
	2	20	100.0	21	12	ADM94731	Adm94731 Human hea
c	3	19	95.0	19	12	ADM94740	Adm94740 Human hea
	4	16	80.0	21	12	ADM94653	Adm94653 Human hea
	5	15	75.0	21	12	ADM94654	Adm94654 Human hea
	6	14.2	71.0	33	6	ABK52211	Abk52211 Synthetic
c	7	14.2	71.0	47	8	ABZ68928	Abz68928 PCR prime
	8	14	70.0	25	9	ACH58106	Ach58106 DNA targe
	9	13.8	69.0	42	2	AAQ87144	Aaq87144 pBR322 or
	10	13.8	69.0	42	2	AAT32725	Aat32725 Oligo TG6
	11	13.8	69.0	42	2	AAT73265	Aat73265 Downstrea
	12	13.8	69.0	42	2	AAT60986	Aat60986 Downstrea
	13	13.8	69.0	42	2	AAV58346	Aav58346 Primer TG
	14	13.8	69.0	42	5	AAC81485	Aac81485 pBR322 or
c	15	13.2	66.0	25	9	ACI03862	Aci03862 Human mic
	16	13.2	66.0	25	9	ACI65798	Aci65798 Human mic
	17	13.2	66.0	27	4	AAH21740	Aah21740 Corynebac
	18	13.2	66.0	43	4	AAA91324	Aaa91324 Rep68 and
	19	13.2	66.0	43	6	AAD36295	Aad36295 Rep68 and
	20	13.2	66.0	43	6	AAD46152	Aad46152 Rep68 and
	21	13.2	66.0	43	6	AAD44614	Aad44614 Rep 68 an
	22	13.2	66.0	43	8	ACC69259	Acc69259 Rep68 and
	23	13.2	66.0	43	10	ADI40307	Adi40307 Rep68 and
	24	13.2	66.0	43	10	ABX96683	Abx96683 Rep68/78
	25	13.2	66.0	43	10	ABX96538	Abx96538 Rep68 and
c	26	13.2	66.0	44	3	AAZ55202	Aaz55202 Neisseria
	27	13.2	66.0	49	2	AAT80499	Aat80499 Hepatoma
c	28	12.8	64.0	21	2	AAV51704	Aav51704 Zea mays
c	29	12.8	64.0	23	3	AAA75395	Aaa75395 Fragment
	30	12.8	64.0	24	8	ABZ58873	Abz58873 Zebrafish
c	31	12.8	64.0	25	9	ACI84537	Aci84537 Human mic
	32	12.8	64.0	29	12	ADO31537	Ado31537 Human CFT
	33	12.8	64.0	30	14	ADY40845	Ady40845 PCR fragm
c	34	12.8	64.0	37	2	AAX55824	Aax55824 PCR prime
c	35	12.8	64.0	39	6	ABA98226	Aba98226 Oligonucl
	36	12.8	64.0	40	2	AAT69484	Aat69484 Plasmid p
c	37	12.8	64.0	40	2	AAT69525	Aat69525 Plasmid p
c	38	12.8	64.0	40	2	AAV51220	Aav51220 Maize pol
	39	12.8	64.0	40	2	AAX88908	Aax88908 Circular
c	40	12.8	64.0	40	2	AAX88950	Aax88950 Circular
	41	12.8	64.0	40	6	ABA98183	Aba98183 Oligonucl
	42	12.8	64.0	40	6	ABA98184	Aba98184 Oligonucl
c	43	12.8	64.0	41	6	ABV75699	Abv75699 Human zin
c	44	12.8	64.0	42	14	AEB08695	Aeb08695 RSV-X low
	45	12.8	64.0	44	14	AEB08694	Aeb08694 RSV-X low

ALIGNMENTS

RESULT 1
ADM94732
ID ADM94732 standard; DNA; 20 BP.
XX
AC ADM94732;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human heat shock protein 27 antisense oligonucleotide SEQ ID NO:82.
XX
KW heat shock protein 27; hsp27; cytostatic; gene therapy;
KW heat shock protein 27 inhibitor; hsp27 inhibitor; cancer; human;
KW antisense oligonucleotide; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO2004030660-A2.
XX
PD 15-APR-2004.
XX
PF 02-OCT-2003; 2003WO-CA001588.
XX
PR 02-OCT-2002; 2002US-0415859P.
PR 18-APR-2003; 2003US-0463952P.
XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI Gleave ME, Rocchi P, Signaevsky M;
XX
DR WPI; 2004-316331/29.
XX
PT New composition comprising a therapeutic agent that reduces the amount of
PT active hsp27 in hsp27 expressing cells exposed to the therapeutic agent,
PT useful in treating cancer, e.g., prostate cancer or a central nervous
PT system malignancy.
XX
PS Claim 6; SEQ ID NO 82; 38pp; English.
XX
CC The present invention describes a composition which comprises a
CC therapeutic agent that reduces the amount of active heat shock protein 27
CC (hsp27) in hsp27 expressing cells exposed to the therapeutic agent. The

```
CC   composition has cytostatic activity, and can be used in gene therapy. The
CC   composition is useful in treating cancer, e.g., prostate, bladder, lung,
CC   breast, pancreatic, colon, skin (for example melanoma), renal or ovarian
CC   cancer or a central nervous system malignancy. The present sequence
CC   represents a human hsp27 antisense oligonucleotide which is used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 20 BP; 2 A; 6 C; 9 G; 3 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 20;  DB 12;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 12;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGGACGCGGCGCTCGGTCAT 20
              ||||||||||||||||||||
Db          1 GGGACGCGGCGCTCGGTCAT 20


RESULT 2
ADM94731
ID   ADM94731 standard; DNA; 21 BP.
XX
AC   ADM94731;
XX
DT   01-JUL-2004  (first entry)
XX
DE   Human heat shock protein 27 antisense oligonucleotide SEQ ID NO:81.
XX
KW   heat shock protein 27; hsp27; cytostatic; gene therapy;
KW   heat shock protein 27 inhibitor; hsp27 inhibitor; cancer; human;
KW   antisense oligonucleotide; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2004030660-A2.
XX
PD   15-APR-2004.
XX
PF   02-OCT-2003; 2003WO-CA001588.
XX
PR   02-OCT-2002; 2002US-0415859P.
PR   18-APR-2003; 2003US-0463952P.
XX
PA   (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI   Gleave ME,  Rocchi P,  Signaevsky M;
XX
DR   WPI; 2004-316331/29.
XX
PT   New composition comprising a therapeutic agent that reduces the amount of
PT   active hsp27 in hsp27 expressing cells exposed to the therapeutic agent,
PT   useful in treating cancer, e.g., prostate cancer or a central nervous
PT   system malignancy.
XX
PS   Claim 5; SEQ ID NO 81; 38pp; English.
XX
CC   The present invention describes a composition which comprises a
CC   therapeutic agent that reduces the amount of active heat shock protein 27
CC   (hsp27) in hsp27 expressing cells exposed to the therapeutic agent. The
CC   composition has cytostatic activity, and can be used in gene therapy. The
CC   composition is useful in treating cancer, e.g., prostate, bladder, lung,
CC   breast, pancreatic, colon, skin (for example melanoma), renal or ovarian
CC   cancer or a central nervous system malignancy. The present sequence
CC   represents a human hsp27 antisense oligonucleotide which is used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 21 BP; 2 A; 6 C; 10 G; 3 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 20;  DB 12;  Length 21;
  Best Local Similarity  100.0%;  Pred. No. 12;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGGACGCGGCGCTCGGTCAT 20
              ||||||||||||||||||||
Db          2 GGGACGCGGCGCTCGGTCAT 21


RESULT 3
ADM94740/c
ID   ADM94740 standard; DNA; 19 BP.
XX
AC   ADM94740;
XX
DT   01-JUL-2004  (first entry)
XX
DE   Human heat shock protein 27 siRNA oligonucleotide SEQ ID NO:90.
XX
KW   heat shock protein 27; hsp27; cytostatic; gene therapy;
KW   heat shock protein 27 inhibitor; hsp27 inhibitor; cancer; human;
KW   short interfering RNA; siRNA; RNA interference; RNAi; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2004030660-A2.
XX
PD   15-APR-2004.
XX
PF   02-OCT-2003; 2003WO-CA001588.
XX
PR   02-OCT-2002; 2002US-0415859P.
PR   18-APR-2003; 2003US-0463952P.
XX
PA   (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI   Gleave ME,  Rocchi P,  Signaevsky M;
XX
DR   WPI; 2004-316331/29.
XX
PT   New composition comprising a therapeutic agent that reduces the amount of
PT   active hsp27 in hsp27 expressing cells exposed to the therapeutic agent,
PT   useful in treating cancer, e.g., prostate cancer or a central nervous
PT   system malignancy.
XX
PS   Claim 10; SEQ ID NO 90; 38pp; English.
XX
CC   The present invention describes a composition which comprises a
CC   therapeutic agent that reduces the amount of active heat shock protein 27
CC   (hsp27) in hsp27 expressing cells exposed to the therapeutic agent. The
CC   composition has cytostatic activity, and can be used in gene therapy. The
CC   composition is useful in treating cancer, e.g., prostate, bladder, lung,
CC   breast, pancreatic, colon, skin (for example melanoma), renal or ovarian
CC   cancer or a central nervous system malignancy. The present sequence
CC   represents a human hsp27 short interfering RNA (siRNA) oligonucleotide
CC   which is used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 3 A; 8 C; 6 G; 0 T; 2 U; 0 Other;

  Query Match            95.0%;  Score 19;  DB 12;  Length 19;
  Best Local Similarity  100.0%;  Pred. No. 34;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GGACGCGGCGCTCGGTCAT 20
              ||||||||||||||||||
Db         19 GGACGCGGCGCTCGGTCAT 1


RESULT 4
ADM94653
ID   ADM94653 standard; DNA; 21 BP.
XX
AC   ADM94653;
XX
DT   01-JUL-2004  (first entry)
XX
```

```
DE   Human heat shock protein 27 antisense oligonucleotide SEQ ID NO:3.
XX
KW   heat shock protein 27; hsp27; cytostatic; gene therapy;
KW   heat shock protein 27 inhibitor; hsp27 inhibitor; cancer; human;
KW   antisense oligonucleotide; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2004030660-A2.
XX
PD   15-APR-2004.
XX
PF   02-OCT-2003; 2003WO-CA001588.
XX
PR   02-OCT-2002; 2002US-0415859P.
PR   18-APR-2003; 2003US-0463952P.
XX
PA   (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI   Gleave ME,  Rocchi P,  Signaevsky M;
XX
DR   WPI; 2004-316331/29.
XX
PT   New composition comprising a therapeutic agent that reduces the amount of
PT   active hsp27 in hsp27 expressing cells exposed to the therapeutic agent,
PT   useful in treating cancer, e.g., prostate cancer or a central nervous
PT   system malignancy.
XX
PS   Claim 5; SEQ ID NO 3; 38pp; English.
XX
CC   The present invention describes a composition which comprises a
CC   therapeutic agent that reduces the amount of active heat shock protein 27
CC   (hsp27) in hsp27 expressing cells exposed to the therapeutic agent. The
CC   composition has cytostatic activity, and can be used in gene therapy. The
CC   composition is useful in treating cancer, e.g., prostate, bladder, lung,
CC   breast, pancreatic, colon, skin (for example melanoma), renal or ovarian
CC   cancer or a central nervous system malignancy. The present sequence
CC   represents a human hsp27 antisense oligonucleotide which is used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 21 BP; 1 A; 7 C; 9 G; 4 T; 0 U; 0 Other;

  Query Match             80.0%;  Score 16;  DB 12;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 8.2e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CGCGGCGCTCGGTCAT 20
              ||||||||||||||||
Db          1 CGCGGCGCTCGGTCAT 16


RESULT 5
ADM94654
ID   ADM94654 standard; DNA; 21 BP.
XX
AC   ADM94654;
XX
DT   01-JUL-2004  (first entry)
XX
DE   Human heat shock protein 27 antisense oligonucleotide SEQ ID NO:4.
XX
KW   heat shock protein 27; hsp27; cytostatic; gene therapy;
KW   heat shock protein 27 inhibitor; hsp27 inhibitor; cancer; human;
KW   antisense oligonucleotide; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2004030660-A2.
XX
PD   15-APR-2004.
XX
PF   02-OCT-2003; 2003WO-CA001588.
XX
PR   02-OCT-2002; 2002US-0415859P.
PR   18-APR-2003; 2003US-0463952P.
XX
PA   (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI   Gleave ME,  Rocchi P,  Signaevsky M;
XX
DR   WPI; 2004-316331/29.
XX
PT   New composition comprising a therapeutic agent that reduces the amount of
PT   active hsp27 in hsp27 expressing cells exposed to the therapeutic agent,
PT   useful in treating cancer, e.g., prostate cancer or a central nervous
PT   system malignancy.
XX
PS   Claim 5; SEQ ID NO 4; 38pp; English.
XX
CC   The present invention describes a composition which comprises a
CC   therapeutic agent that reduces the amount of active heat shock protein 27
CC   (hsp27) in hsp27 expressing cells exposed to the therapeutic agent. The
CC   composition has cytostatic activity, and can be used in gene therapy. The
CC   composition is useful in treating cancer, e.g., prostate, bladder, lung,
CC   breast, pancreatic, colon, skin (for example melanoma), renal or ovarian
CC   cancer or a central nervous system malignancy. The present sequence
CC   represents a human hsp27 antisense oligonucleotide which is used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 21 BP; 4 A; 5 C; 11 G; 1 T; 0 U; 0 Other;

  Query Match             75.0%;  Score 15;  DB 12;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGGACGCGGCGCTCG 15
              |||||||||||||||
Db          7 GGGACGCGGCGCTCG 21


RESULT 6
ABK52211
ID   ABK52211 standard; DNA; 33 BP.
XX
AC   ABK52211;
XX
DT   13-AUG-2002  (first entry)
XX
DE   Synthetic product 2 reverse PCR primer for construction of pASK-MBD.
XX
KW   Mercuric ion; contaminated soil; ground water; hydroponic solution;
KW   irrigation water; waste stream; contaminated aqueous medium;
KW   biological fluid; gastrointestinal tract; chelon protein;
KW   enteric bacteria; toxic metal ion; mercury; cadmium; divalent cation;
KW   heavy metal binding protein; pASK-MBD; PCR; primer; ss.
XX
OS   Synthetic.
XX
PN   WO200230962-A2.
XX
PD   18-APR-2002.
XX
PF   12-OCT-2001; 2001WO-US031819.
XX
PR   12-OCT-2000; 2000US-0240465P.
XX
PA   (UYGE-) UNIV GEORGIA RES FOUND INC.
XX
PI   Summers AO,  Caguiat JJ;
XX
DR   WPI; 2002-435437/46.
XX
PT   Novel non-naturally occurring recombinant DNA molecule encoding a chelon
PT   protein useful for binding divalent cation mercury from contaminated
```

PT soil, water, aqueous medium including biological fluids.
XX
PS Disclosure; Page 24; 42pp; English.
XX
CC The present invention relates to a new non-naturally occurring
CC recombinant DNA molecule comprising a sequence encoding a chelon protein
CC which binds mercuric ions. The invention is useful for recombinantly
CC producing a protein in a host-cell, by infecting or transforming a host
CC cell capable of expressing a chelon coding sequence with a vector
CC comprising a promoter active in the host cell operably linked to a coding
CC region for the protein to produce a recombinant host cell and culturing
CC the recombinant host cell under conditions, where DNA is expressed. The
CC nucleic acid encoding the chelon protein is useful for binding divalent
CC mercuric ions, to take up, sequester and concentrate the heavy metal ions
CC from contaminated soil, ground water, hydroponic solutions or irrigation
CC water of waste streams. The DNA of the invention, when immobilised onto a
CC solid support, is useful for concentrating heavy metal ions from
CC contaminated environment waste streams or contaminated aqueous medium
CC including biological fluids. The nucleic acid, when recombinantly
CC expressed in enteric bacteria (which are nontoxigenic and nonpathogenic),
CC is suitable for use in the in vivo sequestration and elimination of
CC mercuric ion from gastrointestinal tracts of animals or humans exposed to
CC toxic metal ions such as mercury and/or cadmium. The molecules of the
CC invention are also useful in water treatment resins. The nucleic acid of
CC the invention is highly specific and binds divalent cation such as
CC mercury or cadmium with high affinity. The present nucleic acid sequence
CC represents synthetic product 2 reverse PCR primer that was used in the
CC methods of the invention for construction of pASK-MBD vector
XX
SQ Sequence 33 BP; 6 A; 8 C; 12 G; 7 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 6; Length 33;
Best Local Similarity 84.2%; Pred. No. 5.4e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGACGCGGCGCTCGGTCA 19
||| | |||||||||| ||
Db 6 GGGTCTCGGCGCTCGGGCA 24

RESULT 7
ABZ68928/c
ID ABZ68928 standard; DNA; 47 BP.
XX
AC ABZ68928;
XX
DT 28-MAY-2003 (first entry)
XX
DE PCR primer used to amplify a PKS domain DNA sequence.
XX
KW Simvastatin; polyketide synthase; PKS; HMPKSB2; PCR; primer; ss.
XX
OS Unidentified.
XX
PN WO2003010324-A2.
XX
PD 06-FEB-2003.
XX
PF 25-JUL-2002; 2002WO-IN000157.
XX
PR 25-JUL-2001; 2001IN-DE000796.
XX
PA (ITGE-) INT CENT GENETIC ENG & BIOTECHNOLOGY.
XX
PI Ranganathan A;
XX
DR WPI; 2003-248083/24.
XX
PT Preparing simvastatin or its analogs or derivatives, by providing a host
PT having a customized gene encoding a polyketide synthase, and fermenting
PT the host to obtain simvastatin or its analogs or derivatives.
XX
PS Example 1.2.3; Page 21; 40pp; English.
XX
CC The specification describes a method of preparing simvastatin or its
CC analogues or derivatives by biological expression. The method comprises
CC providing a host having a customized gene encoding for a polyketide
CC synthase (PKS), and fermenting the host to obtain simvastatin or its
CC analogues or derivatives. The method is useful for producing simvastatin
CC or its analogues or derivatives. PCR primers ABZ68927-28 were used to
CC amplify a PKS domain DNA sequence. The amplified fragment was used in the
CC construction of the hybrid modular PKS B2 (HMPKSB2), for use in the
CC method of the invention
XX
SQ Sequence 47 BP; 8 A; 14 C; 20 G; 5 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 8; Length 47;
Best Local Similarity 84.2%; Pred. No. 5.4e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGACGCGGCGCTCGGTCA 19
|| |||||||||||| ||
Db 33 GGACCGCGGCGCTCGGCCA 15

RESULT 8
ACH58106
ID ACH58106 standard; DNA; 25 BP.
XX
AC ACH58106;
XX
DT 16-OCT-2003 (first entry)
XX
DE DNA target sequence #7242 useful in array for genetic analyses.
XX
KW Gene expression analysis; array; hybridisation; genetic variation;
KW tag-labelled compound; gene family; in situ hybridisation;
KW library screening; Southern hybridisation; northern hybridisation;
KW dot-blot hybridisation; gene sequence; mutation detection;
KW target sequence; probe; PCR; primer; ss.
XX
OS Unidentified.
XX
PN US2003082596-A1.
XX
PD 01-MAY-2003.
XX
PF 08-AUG-2002; 2002US-00215112.
XX
PR 08-AUG-2001; 2001US-0311040P.
XX
PA (MITT/) MITTMANN M.
XX
PI Mittmann M;
XX
DR WPI; 2003-576608/54.
XX
PT New probe array useful e.g. for monitoring gene expression levels, for
PT analyzing genetic variations, or for hybridizing tag-labeled compounds,
PT comprises multiple nucleic acid probes.
XX
PS Claim 1; SEQ ID NO 7242; 9pp; English.
XX
CC The present invention relates to nucleic acid sequences that are
CC complementary to particular genes, and can be used as probes for a
CC variety of analyses such as gene expression analysis. Each probe
CC comprises 9 or more consecutive nucleotides from at least one of 14936
CC nucleotide sequences defined in the patent, or their perfect sense match,
CC sense mismatch, antisense match or antisense mismatch oligonucleotides.
CC The probes may be used in an array comprising at least 10 distinct
CC nucleic acid probes. The array is useful in monitoring gene expression
CC levels by hybridisation to a DNA library, in analysing genetic
CC variations, and in hybridising tag-labelled compounds. The probes are
CC useful for identifying family members of a gene. The probes are also
CC useful in in situ hybridisations, in screening cDNA or genomic libraries
CC (or derived subclones) for additional clones containing segments of DNA

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CC   that have been previously isolated and sequenced, in Southern, northern,
CC   or dot-blot hybridisation of genomic DNA to identify or detect the
CC   sequence of any gene or detect specific mutations in any gene, and in
CC   mapping the 5' termini of mRNA molecules by primer extensions. The
CC   nucleic acid sequences of the invention are also useful as PCR primers.
CC   The invention provides a large collection of nucleic acid sequences
CC   complementary to particular genes with a wide range of analytical uses.
CC   ACH50865-ACH65260 represent the target sequences of the invention. Note:
CC   The sequence data for this patent was obtained in electronic format
CC   directly from the USPTO web site at seqdata.uspto.gov/psipsDIDEntry.html
XX
SQ   Sequence 25 BP; 4 A; 9 C; 9 G; 3 T; 0 U; 0 Other;

  Query Match             70.0%;  Score 14;  DB 9;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 6.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GGACGCGGCGCTCG 15
              ||||||||||||||
Db          2 GGACGCGGCGCTCG 15


RESULT 9
AAQ87144
ID   AAQ87144 standard; DNA; 42 BP.
XX
AC   AAQ87144;
XX
DT   24-JAN-1996  (first entry)
XX
DE   pBR322 ori downstream amplification primer TG63.
XX
KW   Primer; PCR; amplification; recombinant haemoglobin; alpha subunit;
KW   expression vector; purity; beta subunit; tac promoter; tet gene;
KW   lambda repressor gene; lacI; ss.
XX
OS   Synthetic.
XX
PN   WO9514038-A2.
XX
PD   26-MAY-1995.
XX
PF   15-NOV-1994;   94WO-US013034.
XX
PR   15-NOV-1993;   93US-00153071.
XX
PA   (SOMA-) SOMATOGEN INC.
XX
PI   Milne EE,  Plomer JJ,  Rausch SK,  Hogenson DC,  Ryland JR;
PI   Matthews MH,  Ernst UP,  Houk DE,  Traylor DW,  Williams LR;
PI   Mitchell DJ,  Chivers ML,  Belval TK;
XX
DR   WPI; 1995-200344/26.
XX
PT   Purification of haemoglobin, esp. recombinant haemoglobin - using e.g.
PT   immobilised metal affinity chromatography heating steps, anion exchange
PT   resins and chelating agents.
XX
PS   Example 1; Page 31; 77pp; English.
XX
CC   The primers AAQ87135-50 were used to subclone the haemoglobin alpha and
CC   beta genes into bacterial expression vectors. The vectors thus
CC   constructed were used in methods to produce recombinant haemoglobin which
CC   can be purified to pharmaceutically acceptable levels of purity by the
CC   methods of the specification. This primer binds downstream of the pBR322
CC   origin of replication (ori) at pos. 2380-2404. The primer with primer
CC   TG62 (AAQ87143) is used to amplify the pBR322 ori. The ori is used in the
CC   construction of the expression vector pSGE705. This vector contains two
CC   copies of the haemoglobin alpha subunit gene in tandem, linked to the
CC   beta subunit gene, all under control of the tac promoter (AAQ87136-7).
CC   The plasmid also has inserted the tet gene and the LacI gene for
CC   regulation of the production of haemoglobin
XX
SQ   Sequence 42 BP; 3 A; 12 C; 16 G; 11 T; 0 U; 0 Other;

  Query Match             69.0%;  Score 13.8;  DB 2;  Length 42;
  Best Local Similarity   88.2%;  Pred. No. 8.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 ACGCGGCGCTCGGTCAT 20
              |||| |||||||||| |
Db         16 ACGCTGCGCTCGGTCGT 32


RESULT 10
AAT32725
ID   AAT32725 standard; DNA; 42 BP.
XX
AC   AAT32725;
XX
DT   07-JAN-1997  (first entry)
XX
DE   Oligo TG63 for creation of recombinant haemoglobin.
XX
KW   Haemoglobin; alpha globin; beta globin; Hb; dietary supplement; anaemia;
KW   molecular weight marker; oxygen carrier; transfusion; oxygen delivery;
KW   erythrocyte; nitric oxide; non-oxygenated ligand; therapy; hypertension;
KW   hypotension; septic shock; polymerase chain reaction; primer; amplify;
KW   PCR; ss.
XX
OS   Synthetic.
XX
PN   WO9615151-A1.
XX
PD   23-MAY-1996.
XX
PF   11-MAY-1995;   95WO-US005786.
XX
PR   14-NOV-1994;   94US-00339304.
PR   10-MAY-1995;   95US-00438511.
XX
PA   (SOMA-) SOMATOGEN INC.
XX
PI   Plomer JJ,  Ryland JR,  Matthews MH,  Traylor DW,  Milne EE;
PI   Durfee SL,  Mathews AJ,  Neway JO;
XX
DR   WPI; 1996-259784/26.
XX
PT   Purificn. of haemoglobin soln. from cell lysate by metal affinity
PT   chromatography - opt. followed by anion exchange chromatography and
PT   oxygenation of the soln., partic. useful as therapeutic oxygen carrier.
XX
PS   Example 1; Page 30; 74pp; English.
XX
CC   AAT32717-T32725 represent oligonucleotides used in the creation of the
CC   plasmid pSGE705. This sequence represents the downstream primer for the
CC   pBR322 ori. pSGE705 contains the pBR322 ori, a lacI gene, a di-alpha
CC   globin gene, a tetracycline resistance gene, and a beta globin gene. A
CC   lysate of bacteria transformed with pSGE705 is then used in the method of
CC   the invention for production of a haemoglobin (Hb) solution. In the
CC   method, a Hb-containing lysate is applied to an immobilised metal
CC   affinity chromatography resin loaded with a divalent ion. The resin is
CC   washed with a solution containing a competitive ligand, then washed with
CC   a buffer to remove the competitive ligand. The solution is the eluted to
CC   recover a partially purified Hb solution. The Hb solution produced can be
CC   used as dietary supplements to provide iron, as molecular weight markers,
CC   and as oxygen carriers for transfusions. Also, the solution can be used
CC   to treat anaemia, to deliver oxygen to cell cultures or, in vivo, to
CC   tissues downstream of occlusions that cannot be reached by erythrocytes.
CC   The Hb can also function to deliver or remove nitric oxide (NO) or non-
CC   oxygenated ligands, as a drug delivery vehicle, and to remove oxygen from
CC   solutions. The delivery of NO is useful as therapy in cases of
CC   hypertension, while removal of excess NO can be used to treat hypotension
CC   and septic shock. The method can be applied to lysates of erythrocytes,
CC   or of recombinant cells, and is able to remove the large amounts of
CC   contaminants present in recombinant Hb solutions
```

```
XX
SQ   Sequence 42 BP; 3 A; 12 C; 16 G; 11 T; 0 U; 0 Other;

  Query Match            69.0%;  Score 13.8;  DB 2;  Length 42;
  Best Local Similarity  88.2%;  Pred. No. 8.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 ACGCGGCGCTCGGTCAT 20
              |||| |||||||||| |
Db         16 ACGCTGCGCTCGGTCGT 32


RESULT 11
AAT73265
ID   AAT73265 standard; DNA; 42 BP.
XX
AC   AAT73265;
XX
DT   11-SEP-1997  (first entry)
XX
DE   Downstream primer TG63 to amplify pBR322 origin of replication.
XX
KW   Linker; haemoglobin; alpha domain; beta domain; red blood cell;
KW   haemorrhage; trauma; anaemia; surgery; oxygen carrying capacity.
XX
OS   Synthetic.
XX
PN   WO9640920-A1.
XX
PD   19-DEC-1996.
XX
PF   06-JUN-1996;   96WO-US010420.
XX
PR   07-JUN-1995;   95US-00487431.
XX
PA   (SOMA-) SOMATOGEN INC.
XX
PI   Trimble SP,  Anderson DC,  Mathews AJ,  Anthony-Cahill S;
PI   Marquardt DA,  Madril DG,  Kerwin BA,  Epp JK;
XX
DR   WPI; 1997-052322/05.
XX
PT   Globin-like polypeptide comprising 2 di:alpha domains - useful as red
PT   blood cell substitute, e.g. in treatment of haemorrhage(s), trauma(s),
PT   anaemia(s) and in surgery.
XX
PS   Example 1; Page 21; 61pp; English.
XX
CC   The invention relates to a globin-like polypeptide comprising 2 dialpha
CC   domains preferably linked by a peptide linker of 7 or 14 amino acids,
CC   such as AAW22221-3, attached to other globin-like molecules, e.g. beta-
CC   globin molecules. The primers AAT73264-5 were used to amplify the origin
CC   of replication from the plasmid pBR322, in order to construct a plasmid
CC   for expression of the novel haemoglobin-like protein. This primer binds
CC   to nucleotides 2380-2404 of the ori sequence. The amplified fragment was
CC   ligated to a fragment containing the tet resistance gene from plasmid
CC   pSELECT-1 (Promega). These fragments were inserted into pUC19 to generate
CC   plasmid pSGE507. Into pSGE507, a fragment containing the alpha and beta
CC   haemoglobin chains was inserted as was a fragment encoding a linked di-
CC   alpha chain. The final construct was named pSGE513. The haemoglobin-like
CC   proteins and compositions containing them can be used as red blood cell
CC   substitutes, e.g. for treating haemorrhages, traumas, anaemias and
CC   surgeries where fluid volume and/or oxygen carrying capacity must be
CC   replaced
XX
SQ   Sequence 42 BP; 3 A; 12 C; 16 G; 11 T; 0 U; 0 Other;

  Query Match            69.0%;  Score 13.8;  DB 2;  Length 42;
  Best Local Similarity  88.2%;  Pred. No. 8.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 ACGCGGCGCTCGGTCAT 20
              |||| |||||||||| |
Db         16 ACGCTGCGCTCGGTCGT 32


RESULT 12
AAT60986
ID   AAT60986 standard; DNA; 42 BP.
XX
AC   AAT60986;
XX
DT   28-OCT-1997  (first entry)
XX
DE   Downstream primer for pBR322 ori positions 2380-2404.
XX
KW   Preparation; construction; plasmid; pSGE705; pBR; globin;
KW   replication origin; tetracycline resistance; di-alpha; di-beta;
KW   tac promoter; LacI; primer; polymerase chain reaction; PCR;
KW   amplification; ss.
XX
OS   Synthetic.
XX
PN   WO9704110-A1.
XX
PD   06-FEB-1997.
XX
PF   12-JUL-1996;   96WO-US011600.
XX
PR   14-JUL-1995;   95US-0001179P.
XX
PA   (SOMA-) SOMATOGEN INC.
XX
PI   Weickert MJ,  Glascock CB;
XX
DR   WPI; 1997-132648/12.
XX
PT   Prokaryotic cell contg. plasmid including regulatable expression unit -
PT   for heterologous protein, and chromosomal gene encoding regulator of this
PT   unit controlled by strong promoter, provides tight control of expression.
XX
PS   Example 1; Page 15; 60pp; English.
XX
CC   The present sequence was used in the preparation of the plasmid pSGE705,
CC   which has the pBR origin of replication, tetracycline resistance gene,
CC   the di-alpha and di-beta globin genes, tac promoter and LacI
XX
SQ   Sequence 42 BP; 3 A; 12 C; 16 G; 11 T; 0 U; 0 Other;

  Query Match            69.0%;  Score 13.8;  DB 2;  Length 42;
  Best Local Similarity  88.2%;  Pred. No. 8.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 ACGCGGCGCTCGGTCAT 20
              |||| |||||||||| |
Db         16 ACGCTGCGCTCGGTCGT 32


RESULT 13
AAV58346
ID   AAV58346 standard; DNA; 42 BP.
XX
AC   AAV58346;
XX
DT   20-NOV-1998  (first entry)
XX
DE   Primer TG63 for haemoglobin mutant coding sequence.
XX
KW   PCR primer; haemoglobin mutant; N-terminal methylation; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US5811264-A.
XX
PD   22-SEP-1998.
```

XX
PF 29-FEB-1996; 96US-00609271.
XX
PR 27-JAN-1994; 94US-00188374.
XX
PA (SOMA-) SOMATOGEN INC.
XX
PI Levine JD, Aitken JF, Apostol IZ, Lippincott JA;
XX
DR WPI; 1998-530871/45.
XX
PT Mutated protein without proline at position 4 - to eliminate N-terminal
PT methylation.
XX
PS Example 1; Col 15; 26pp; English.
XX
CC This sequence represents a primer for a mutated haemoglobin of the
CC invention. The invention relates to a mutated variant of a protein that
CC has proline at position 4 and is at least partially methylated on its N
CC terminus when expressed in bacteria, the variant has an amino acid other
CC than proline at position 4 and is not methylated on its N-terminus when
CC expressed in bacteria. Recombinant haemoglobin that is not N-terminally
CC methylated might avoid the immunological consequences implied by such
CC methylation
XX
SQ Sequence 42 BP; 3 A; 12 C; 16 G; 11 T; 0 U; 0 Other;

Query Match 69.0%; Score 13.8; DB 2; Length 42;
Best Local Similarity 88.2%; Pred. No. 8.3e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 ACGCGGCGCTCGGTCAT 20
|||| |||||||||| |
Db 16 ACGCTGCGCTCGGTCGT 32

RESULT 14
AAC81485
ID AAC81485 standard; DNA; 42 BP.
XX
AC AAC81485;
XX
DT 28-FEB-2001 (first entry)
XX
DE pBR322 ori downstream PCR primer, SEQ ID NO:21.
XX
KW Recombinant human haemoglobin; rHb1.1; bacterial expression;
KW N-terminal methionine methylation signal; demethylation;
KW Escherichia coli; non-immunogenic; pharmaceutical composition;
KW PCR primer; ss.
XX
OS Synthetic.
XX
PN US6140071-A.
XX
PD 31-OCT-2000.
XX
PF 27-JAN-1994; 94US-00188374.
XX
PR 27-JAN-1994; 94US-00188374.
XX
PA (SOMA-) SOMATOGEN INC.
XX
PI Aitken JF, Apostol IZ, Levine JD, Lippincott JA;
XX
DR WPI; 2001-048957/06.
XX
PT Decreasing methylation of an N-terminus protein, especially hemoglobin
PT having proline at amino acid position 4, useful for producing
PT demethylated proteins for treating diseases, by altering this amino acid
PT to a non-proline residue.
XX
PS Example 1; Col 15; 26pp; English.
XX
CC The invention relates to a method of decreasing the amount of N-terminal
CC methionine methylation on a protein expressed in a bacterium. The
CC bacterial methyltransferase which directs N-terminal methionine
CC methylation recognises proteins which have a proline residue at position
CC 4 (e.g., the bacterial ribosomal protein L16 and the bacterial chemotaxis
CC protein CheZ). The method comprises introducing mutations into the DNA
CC encoding the protein so that residue 4 is a non-proline residue, thereby
CC reducing the degree of N-terminal methylation when the protein is
CC expressed in a bacterium. The method is useful for decreasing methylation
CC of a protein, particularly a recombinantly produced protein. The
CC demethylated protein can be used in a pharmaceutical composition for the
CC treatment of a disease but with less likelihood of eliciting an
CC immunological response. These demethylated proteins may be used as
CC therapeutic agent for the treatment and/or amelioration of disease or
CC symptoms associated with a disease. The exemplifications describe the
CC expression of a recombinant human haemoglobin construct (rHb1.1) in
CC Escherichia coli, and its modification such that residue 4 of the di-
CC alpha chain of the recombinant haemoglobin is altered from proline to a
CC non-proline residue. The present sequence represents a PCR primer used in
CC the exemplifications of the invention
XX
SQ Sequence 42 BP; 3 A; 12 C; 16 G; 11 T; 0 U; 0 Other;

Query Match 69.0%; Score 13.8; DB 5; Length 42;
Best Local Similarity 88.2%; Pred. No. 8.3e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 ACGCGGCGCTCGGTCAT 20
|||| |||||||||| |
Db 16 ACGCTGCGCTCGGTCGT 32

RESULT 15
ACI03862/c
ID ACI03862 standard; DNA; 25 BP.
XX
AC ACI03862;
XX
DT 13-OCT-2003 (first entry)
XX
DE Human microarray DNA oligonucleotide SEQ ID NO 3853.
XX
KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.
XX
OS Homo sapiens.
XX
PN US2003104410-A1.
XX
PD 05-JUN-2003.
XX
PF 15-MAR-2002; 2002US-00098263.
XX
PR 16-MAR-2001; 2001US-0276759P.
XX
PA (AFFY-) AFFYMETRIX INC.
XX
PI Mittmann MP;
XX
DR WPI; 2003-567953/53.
XX
PT New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX
PS Claim 1; SEQ ID NO 3853; 9pp; English.
XX
CC The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used

CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying biallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in in situ hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.goc/sequence.html
XX
SQ Sequence 25 BP; 6 A; 8 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 66.0%; Score 13.2; DB 9; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.6e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          2 GGACGCGGCGCTCGGTCA 19
              |||| || || |||||||
Db         24 GGACTCGTCGGTCGGTCA 7
```

Search completed: December 13, 2005, 13:29:55
Job time : 263 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 12:30:55 ; Search time 1918 Seconds
(without alignments)
487.874 Million cell updates/sec

Title: US-10-605-498-82
Perfect score: 20
Sequence: 1 gggacgcggcgctcggtcat 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 179606

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	13.8	69.0	36	3	BM050289	BM050289 603632506
	2	13.6	68.0	49	7	CO780197	CO780197 BL009A_A0
	3	13.4	67.0	49	3	BI760726	BI760726 603044726
	4	13.2	66.0	37	2	BG166786	BG166786 602339133
c	5	12.8	64.0	32	2	BF131807	BF131807 601820724
	6	12.8	64.0	42	3	BI553162	BI553162 603197760
c	7	12.8	64.0	50	1	AU105403	AU105403 AU105403
c	8	12.8	64.0	50	1	AU105404	AU105404 AU105404
c	9	12.8	64.0	50	1	AU105405	AU105405 AU105405
c	10	12.8	64.0	50	1	AU105406	AU105406 AU105406
c	11	12.6	63.0	50	1	AU107987	AU107987 AU107987
c	12	12.6	63.0	50	1	AU107995	AU107995 AU107995
	13	12.4	62.0	26	10	AG203073	AG203073 Pan trogl
c	14	12.4	62.0	50	1	AU105647	AU105647 AU105647
c	15	12.4	62.0	50	1	AU105649	AU105649 AU105649
c	16	12.2	61.0	28	1	AI287864	qv07d12.x
	17	12.2	61.0	38	2	BF525570	BF525570 602069675
	18	12.2	61.0	45	9	AQ026252	AQ026252 1(3)L3130
c	19	12.2	61.0	50	1	AU107551	AU107551 AU107551
c	20	12	60.0	31	1	AA867755	AA867755 vx16b08.r
c	21	12	60.0	31	10	CZ169504	CZ169504 G050C04 G
	22	12	60.0	49	1	AI339668	AI339668 qk63c12.x
	23	12	60.0	50	1	AU104529	AU104529 AU104529
	24	12	60.0	50	1	AU104530	AU104530 AU104530
	25	12	60.0	50	1	AU105685	AU105685 AU105685
c	26	11.8	59.0	37	1	AA765049	AA765049 nz78b02.s
c	27	11.8	59.0	40	9	CC940970	CC940970 01S0630-0
c	28	11.8	59.0	45	9	BH913356	BH913356 3526_1_39
c	29	11.8	59.0	47	10	CL639088	CL639088 G080A08 G
	30	11.8	59.0	48	9	CC183531	CC183531 XE344 Bay
c	31	11.8	59.0	49	10	CL212525	CL212525 G043F09 G
c	32	11.8	59.0	50	1	AU102922	AU102922 AU102922
c	33	11.8	59.0	50	1	AU104465	AU104465 AU104465
c	34	11.8	59.0	50	1	AU106742	AU106742 AU106742
	35	11.6	58.0	36	11	DR31K11T	AL977010 Danio rer
c	36	11.6	58.0	38	6	CF296430	CF296430 30DGS--06
c	37	11.6	58.0	42	10	CL301794	CL301794 P002A12 G
c	38	11.6	58.0	43	7	CV066602	CV066602 WNEL6a11
	39	11.6	58.0	44	9	AZ875839	AZ875839 2M0190O06
c	40	11.6	58.0	50	1	AU102349	AU102349 AU102349
c	41	11.6	58.0	50	1	AU102706	AU102706 AU102706
c	42	11.6	58.0	50	1	AU104699	AU104699 AU104699
c	43	11.6	58.0	50	1	AU104786	AU104786 AU104786
c	44	11.6	58.0	50	1	AU104787	AU104787 AU104787
c	45	11.6	58.0	50	1	AU104788	AU104788 AU104788

ALIGNMENTS

RESULT 1
BM050289
LOCUS BM050289 36 bp mRNA linear EST 07-NOV-2001
DEFINITION 603632506F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:5423352 5', mRNA sequence.
ACCESSION BM050289
VERSION BM050289.1 GI:16779556
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 36)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1882 row: k column: 01
High quality sequence stop: 33.
FEATURES Location/Qualifiers
source 1. .36
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5423352"
/tissue_type="normal pigmented retinal epithelium"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_43"
/note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library. |"

```
ORIGIN

  Query Match             69.0%;  Score 13.8;  DB 3;  Length 36;
  Best Local Similarity   88.2%;  Pred. No. 8.6e+04;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GGGACGCGGCGCTCGGT 17
              ||| |||||||||| ||
Db         19 GGGGCGCGGCGCTCCGT 35


RESULT 2
CO780197
LOCUS       CO780197                  49 bp    mRNA    linear   EST 05-AUG-2004
DEFINITION  BL009A_A05 6-Day Axolotl Tail Blastema (6DAxBL) Ambystoma mexicanum
            cDNA 5' similar to hypothetical protein, mRNA sequence.
ACCESSION   CO780197
VERSION     CO780197.1  GI:50996177
KEYWORDS    EST.
SOURCE      Ambystoma mexicanum (axolotl)
  ORGANISM  Ambystoma mexicanum
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
            Ambystoma.
REFERENCE   1  (bases 1 to 49)
  AUTHORS   Habermann,B., Bebin,A.G., Herklotz,S., Volkmer,M., Eckelt,K.,
            Pehlke,K., Epperlein,H.H., Schackert,H.K., Wiebe,G. and Tanaka,E.M.
  TITLE     An Ambystoma mexicanum EST sequencing project: Analysis of 17,352
            expressed sequence tags from embryonic and regenerating blastema
            cDNA libraries
  JOURNAL   Genome Biol. (2004) In press
COMMENT     Contact: Elly M. Tanaka
            Tanaka Lab
            Max Planck Institute of Molecular Cell Biology and Genetics,
            Dresden
            Pfotenhauerstrasse 108,01307 Dresden, Germany
            Tel: 0049 351 210 2620
            Fax: 0049 351 210 1489
            Email: tanaka@mpi-cbg.de
            Plate: BL009A  row: 05  column: A
            Seq primer: GCA CAT TAG GCC TAT TTA GGT GAC A.
FEATURES             Location/Qualifiers
     source          1. .49
                     /organism="Ambystoma mexicanum"
                     /mol_type="mRNA"
                     /db_xref="taxon:8296"
                     /tissue_type="Tail Blastema"
                     /cell_type="regenerating tail blastema"
                     /clone_lib="6-Day Axolotl Tail Blastema (6DAxBL)"
                     /note="Vector: pCMVSport6; Site_1: NotI; Site_2: SalI;
                     Unnormalized cDNA plasmid library prepared by Invitrogen.
                     Size fractionated mRNA was polydT primed and cloned into
                     NotI-SalI site of pCMVSport6. Bacterial host is
                     EMDH10B-TONA. Average insert size is 1.67 kB.
                     TAG_LIB=6DAxBL"
ORIGIN

  Query Match             68.0%;  Score 13.6;  DB 7;  Length 49;
  Best Local Similarity   80.0%;  Pred. No. 1e+05;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GGGACGCGGCGCTCGGTCAT 20
              |||  |||| ||||||| ||
Db          7 GGGCAGCGGTGCTCGGTGAT 26


RESULT 3
BI760726
LOCUS       BI760726                  49 bp    mRNA    linear   EST 25-SEP-2001
DEFINITION  603044726F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5185086 5',
            mRNA sequence.
ACCESSION   BI760726
VERSION     BI760726.1  GI:15752304
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 49)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11462  row: c  column: 07.
FEATURES             Location/Qualifiers
     source          1. .49
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5185086"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_116"
                     /note="Organ: pooled colon, kidney, stomach; Vector:
                     pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
                     source anonymous pool of 3 colons, age 26 yo male, 49 yo
                     female, 71 yo male colon; 46 yo male kidney, and pool of 2
                     stomachs, 62 yo male and 70 yo female.  Library is
                     oligo-dT primed and  directionally cloned (EcoRV site is
                     destroyed upon cloning).  Average insert size 1.4 kb,
                     insert size range 1-3 kb.  Library is normalized and
                     enriched for full-length clones and was constructed by C.
                     Gruber  (Invitrogen).  Research Genetics tracking code
                     023. Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             67.0%;  Score 13.4;  DB 3;  Length 49;
  Best Local Similarity   93.3%;  Pred. No. 1.3e+05;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 ACGCGGCGCTCGGTC 18
              | ||||||||||||||
Db         31 AAGCGGCGCTCGGTC 45


RESULT 4
BG166786
LOCUS       BG166786                  37 bp    mRNA    linear   EST 06-FEB-2001
DEFINITION  602339133F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:4446993 5',
            mRNA sequence.
ACCESSION   BG166786
VERSION     BG166786.1  GI:12673489
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 37)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM10227 row: a column: 10
High quality sequence stop: 37.

FEATURES Location/Qualifiers
source 1. .37
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4446993"
/tissue_type="hypernephroma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_89"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.3 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 66.0%; Score 13.2; DB 2; Length 37;
Best Local Similarity 83.3%; Pred. No. 1.6e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGACGCGGCGCTCGGTC 18
|| || ||||||||| ||
Db 12 GGAACCCGGCGCTCGTTC 29

RESULT 5
BF131807/c
LOCUS BF131807 32 bp mRNA linear EST 24-OCT-2000
DEFINITION 601820724F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052596 5', mRNA sequence.
ACCESSION BF131807
VERSION BF131807.1 GI:10970847
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 32)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCM889 row: p column: 05
High quality sequence start: 8
High quality sequence stop: 30.

FEATURES Location/Qualifiers
source 1. .32
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4052596"
/tissue_type="hypernephroma"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_58"
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.35 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

ORIGIN

Query Match 64.0%; Score 12.8; DB 2; Length 32;
Best Local Similarity 87.5%; Pred. No. 2.5e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CGCGGCGCTCGGTCAT 20
||| |||||||||| |
Db 27 CGCTGCGCTCGGTCGT 12

RESULT 6
BI553162
LOCUS BI553162 42 bp mRNA linear EST 05-SEP-2001
DEFINITION 603197760F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5277350 5', mRNA sequence.
ACCESSION BI553162
VERSION BI553162.1 GI:15440474
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 42)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM11700 row: g column: 15
High quality sequence stop: 42.

FEATURES Location/Qualifiers
source 1. .42
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5277350"
/tissue_type="hippocampus"
/lab_host="DH10B"
/clone_lib="NIH_MGC_95"
/note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 64.0%; Score 12.8; DB 3; Length 42;
Best Local Similarity 87.5%; Pred. No. 2.4e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGGACGCGGCGCTCGG 16
| ||||||| ||||||

```
Db          8 GAGACGCGGAGCTCGG 23


RESULT 7
AU105403/c
LOCUS       AU105403                 50 bp    mRNA    linear   EST 28-JAN-2004
DEFINITION  AU105403 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            CAS05957, mRNA sequence.
ACCESSION   AU105403
VERSION     AU105403.1  GI:13554924
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
            Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
            Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
  TITLE     Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
  JOURNAL   EMBO Rep. 2 (5), 388-393 (2001)
   PUBMED   11375929
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
            Sugano,S. Construction and characterization of a full
            length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
            149-156 (1997).
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CAS05957"
                     /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN

  Query Match             64.0%;  Score 12.8;  DB 1;  Length 50;
  Best Local Similarity   87.5%;  Pred. No. 2.3e+05;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 GGACGCGGCGCTCGGT 17
              |||||| ||||||| |
Db         42 GGACGCAGCGCTCGCT 27


RESULT 8
AU105404/c
LOCUS       AU105404                 50 bp    mRNA    linear   EST 28-JAN-2004
DEFINITION  AU105404 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            HRC10340, mRNA sequence.
ACCESSION   AU105404
VERSION     AU105404.1  GI:13554925
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
            Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
            Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
  TITLE     Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
  JOURNAL   EMBO Rep. 2 (5), 388-393 (2001)
   PUBMED   11375929
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
            Sugano,S. Construction and characterization of a full
            length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
            149-156 (1997).
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="HRC10340"
                     /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN

  Query Match             64.0%;  Score 12.8;  DB 1;  Length 50;
  Best Local Similarity   87.5%;  Pred. No. 2.3e+05;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 GGACGCGGCGCTCGGT 17
              |||||| ||||||| |
Db         48 GGACGCAGCGCTCGCT 33


RESULT 9
AU105405/c
LOCUS       AU105405                 50 bp    mRNA    linear   EST 28-JAN-2004
DEFINITION  AU105405 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            ZRV61110, mRNA sequence.
ACCESSION   AU105405
VERSION     AU105405.1  GI:13554926
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
            Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
            Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
  TITLE     Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
  JOURNAL   EMBO Rep. 2 (5), 388-393 (2001)
   PUBMED   11375929
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
            Sugano,S. Construction and characterization of a full
            length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
            149-156 (1997).
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="ZRV61110"
                     /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN

  Query Match             64.0%;  Score 12.8;  DB 1;  Length 50;
  Best Local Similarity   87.5%;  Pred. No. 2.3e+05;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 GGACGCGGCGCTCGGT 17
              |||||| ||||||| |
Db         42 GGACGCAGCGCTCGCT 27
```

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RESULT 10
AU105406/c
LOCUS       AU105406                  50 bp    mRNA    linear   EST 28-JAN-2004
DEFINITION  AU105406 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            ADSE01811, mRNA sequence.
ACCESSION   AU105406
VERSION     AU105406.1  GI:13554927
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
            Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
            Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
  TITLE     Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
  JOURNAL   EMBO Rep. 2 (5), 388-393 (2001)
   PUBMED   11375929
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
            Sugano,S. Construction and characterization of a full
            length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
            149-156 (1997).
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="ADSE01811"
                     /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN

  Query Match             64.0%;  Score 12.8;  DB 1;  Length 50;
  Best Local Similarity   87.5%;  Pred. No. 2.3e+05;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 GGACGCGGCGCTCGGT 17
              |||||| ||||||| |
Db         16 GGACGCAGCGCTCGCT 1


RESULT 11
AU107987/c
LOCUS       AU107987                  50 bp    mRNA    linear   EST 28-JAN-2004
DEFINITION  AU107987 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            CAS04356, mRNA sequence.
ACCESSION   AU107987
VERSION     AU107987.1  GI:13557509
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
            Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
            Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
  TITLE     Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
  JOURNAL   EMBO Rep. 2 (5), 388-393 (2001)
   PUBMED   11375929
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
            Sugano,S. Construction and characterization of a full
            length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
            149-156 (1997).
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CAS04356"
                     /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN

  Query Match             63.0%;  Score 12.6;  DB 1;  Length 50;
  Best Local Similarity   78.9%;  Pred. No. 2.9e+05;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GGGACGCGGCGCTCGGTCA 19
              ||| |||||||| | | ||
Db         49 GGGCCGCGGCGCGCCGACA 31


RESULT 12
AU107995/c
LOCUS       AU107995                  50 bp    mRNA    linear   EST 28-JAN-2004
DEFINITION  AU107995 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            KAIA2600, mRNA sequence.
ACCESSION   AU107995
VERSION     AU107995.1  GI:13557517
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
            Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
            Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
  TITLE     Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
  JOURNAL   EMBO Rep. 2 (5), 388-393 (2001)
   PUBMED   11375929
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
            Sugano,S. Construction and characterization of a full
            length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
            149-156 (1997).
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="KAIA2600"
                     /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN

  Query Match             63.0%;  Score 12.6;  DB 1;  Length 50;
  Best Local Similarity   78.9%;  Pred. No. 2.9e+05;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GGGACGCGGCGCTCGGTCA 19
              ||| |||||||| | | ||
Db         45 GGGCCGCGGCGCGCCGACA 27


RESULT 13
```

```
AG203073
LOCUS       AG203073                 26 bp    DNA     linear   GSS 06-MAR-2004
DEFINITION  Pan troglodytes DNA, clone: RP43-087B01.T7, genomic survey
            sequence.
ACCESSION   AG203073
VERSION     AG203073.1  GI:45235248
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pan.
REFERENCE   1
  AUTHORS   Park,H., Kim,Y., Kim,S.; Han,Y., Woo,T., Park,K., Eun,C.J.,
            Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
  TITLE     BAC end sequences of Library RP-43
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 26)
  AUTHORS   Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
            Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
            Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC);
            52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
            (E-mail:redstone@mail.kribb.re.kr, URL:http://phs.grc.kribb.re.kr/,
            Tel:82-42-866-7181, Fax:82-42-860-4409)
COMMENT     Clones are derived from the chimpanzee BAC library RP-43 This BAC
            end was generated during the R&D process and may have higher chance
            of clone tracking errors.
             PRIMERS
                 Sequencing: T7
             LIBRARY
                 Vector    : pBACe3.6
                 R.Site 1  : EcoRI
                 R.Site 2  : EcoRI.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
                     /clone="RP43-087B01.T7"
                     /sex="male"
                     /cell_type="lymphocytes"
                     /clone_lib="RP-43 Chimpanzee Male BAC Library"
ORIGIN

  Query Match             62.0%;  Score 12.4;  DB 10;  Length 26;
  Best Local Similarity   92.9%;  Pred. No. 3.9e+05;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGGACGCGGCGCTC 14
              ||||| ||||||||
Db          1 GGGACTCGGCGCTC 14


RESULT 14
AU105647/c
LOCUS       AU105647                 50 bp    mRNA    linear   EST 28-JAN-2004
DEFINITION  AU105647 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            HSI00961, mRNA sequence.
ACCESSION   AU105647
VERSION     AU105647.1  GI:13555168
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
            Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
            Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
  TITLE     Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
  JOURNAL   EMBO Rep. 2 (5), 388-393 (2001)
  PUBMED    11375929
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
            Sugano,S. Construction and characterization of a full
            length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
            149-156 (1997).
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="HSI00961"
                     /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN

  Query Match             62.0%;  Score 12.4;  DB 1;  Length 50;
  Best Local Similarity   92.9%;  Pred. No. 3.5e+05;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGGACGCGGCGCTC 14
              | ||||||||||||
Db         17 GTGACGCGGCGCTC 4


RESULT 15
AU105649/c
LOCUS       AU105649                 50 bp    mRNA    linear   EST 28-JAN-2004
DEFINITION  AU105649 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            HSI02850, mRNA sequence.
ACCESSION   AU105649
VERSION     AU105649.1  GI:13555170
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
            Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
            Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
  TITLE     Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
  JOURNAL   EMBO Rep. 2 (5), 388-393 (2001)
  PUBMED    11375929
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
            Sugano,S. Construction and characterization of a full
            length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
            149-156 (1997).
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="HSI02850"
                     /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN

  Query Match             62.0%;  Score 12.4;  DB 1;  Length 50;
  Best Local Similarity   92.9%;  Pred. No. 3.5e+05;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy          1 GGGACGCGGCGCTC 14
              |||||||||||||
Db         17 GTGACGCGGCGCTC 4
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Search completed: December 13, 2005, 14:30:26
Job time : 1921 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 13:16:54 ; Search time 94 Seconds
(without alignments)
378.205 Million cell updates/sec

Title: US-10-605-498-82
Perfect score: 20
Sequence: 1 gggacgcggcgctcggtcat 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 1299706

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
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4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	14.2	71.0	33	3	US-09-977-137A-16	Sequence 16, Appl
c	2	14	70.0	25	3	US-09-396-196G-42173	Sequence 42173, A
c	3	13.8	69.0	25	3	US-09-396-196G-46323	Sequence 46323, A
c	4	13.8	69.0	25	3	US-09-396-196G-46324	Sequence 46324, A
c	5	13.8	69.0	25	3	US-09-396-196G-46335	Sequence 46335, A
	6	13.8	69.0	42	2	US-08-153-071-14	Sequence 14, Appl
	7	13.8	69.0	42	2	US-08-609-271-21	Sequence 21, Appl
	8	13.8	69.0	42	2	US-08-438-511-14	Sequence 14, Appl
	9	13.8	69.0	42	2	US-08-487-431-17	Sequence 17, Appl
	10	13.8	69.0	42	3	US-08-188-374-21	Sequence 21, Appl
	11	13.8	69.0	42	3	US-08-973-629-17	Sequence 17, Appl
	12	13.2	66.0	25	3	US-09-396-196G-53301	Sequence 53301, A
	13	13	65.0	20	3	US-09-046-858A-19	Sequence 19, Appl
	14	13	65.0	20	3	US-09-450-515-19	Sequence 19, Appl
	15	13	65.0	20	3	US-10-206-654-19	Sequence 19, Appl
c	16	12.8	64.0	37	3	US-08-944-410-47	Sequence 47, Appl
	17	12.8	64.0	40	2	US-08-425-684-86	Sequence 86, Appl
c	18	12.8	64.0	40	2	US-08-425-684-128	Sequence 128, App
	19	12.8	64.0	40	2	US-08-675-502-86	Sequence 86, Appl
c	20	12.8	64.0	40	2	US-08-675-502-128	Sequence 128, App
	21	12.8	64.0	40	3	US-09-245-802-86	Sequence 86, Appl
c	22	12.8	64.0	40	3	US-09-245-802-128	Sequence 128, App
	23	12.6	63.0	20	3	US-10-131-827-8773	Sequence 8773, Ap
c	24	12.6	63.0	24	3	US-09-540-014-35	Sequence 35, Appl
c	25	12.6	63.0	24	3	US-09-164-210-12	Sequence 12, Appl
c	26	12.6	63.0	24	3	US-09-538-864-14	Sequence 14, Appl
c	27	12.6	63.0	24	3	US-10-091-841A-35	Sequence 35, Appl
c	28	12.6	63.0	25	3	US-09-396-196G-40648	Sequence 40648, A
c	29	12.6	63.0	30	3	US-09-319-648-52	Sequence 52, Appl
	30	12.6	63.0	30	9	5240848-8	Patent No. 5240848
c	31	12.6	63.0	39	2	US-08-943-915-30	Sequence 30, Appl
	32	12.4	62.0	20	2	US-08-182-175A-9	Sequence 9, Appli
	33	12.4	62.0	20	2	US-08-474-633A-16	Sequence 16, Appl
	34	12.4	62.0	20	3	US-08-823-771-16	Sequence 16, Appl
	35	12.4	62.0	20	6	PCT-US92-06412-9	Sequence 9, Appli
c	36	12.4	62.0	25	3	US-09-396-196G-41065	Sequence 41065, A
c	37	12.4	62.0	25	3	US-09-396-196G-46162	Sequence 46162, A
c	38	12.4	62.0	25	3	US-09-396-196G-46163	Sequence 46163, A
	39	12.4	62.0	45	2	US-08-753-054-9	Sequence 9, Appli
	40	12.2	61.0	21	3	US-09-158-863C-38	Sequence 38, Appl
c	41	12.2	61.0	22	3	US-09-589-560B-58	Sequence 58, Appl
c	42	12.2	61.0	22	3	US-09-589-560B-62	Sequence 62, Appl
c	43	12.2	61.0	25	3	US-09-396-196G-25195	Sequence 25195, A
c	44	12.2	61.0	25	3	US-09-396-196G-49392	Sequence 49392, A
	45	12.2	61.0	34	3	US-09-487-558B-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-977-137A-16
; Sequence 16, Application US/09977137A
; Patent No. 6750042
; GENERAL INFORMATION:
; APPLICANT: Summers, Anne O.
; APPLICANT: Caguiat, Jonathan
; TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 79-00
; CURRENT APPLICATION NUMBER: US/09/977,137A
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/240,465
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-977-137A-16

Query Match 71.0%; Score 14.2; DB 3; Length 33;
Best Local Similarity 84.2%; Pred. No. 3e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db          6 GGGTCTCGGCGCTCGGGCA 24
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RESULT 2
US-09-396-196G-42173/c
; Sequence 42173, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678

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;  PRIOR FILING DATE: 1998-09-17
;  NUMBER OF SEQ ID NOS: 127806
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 42173
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-09-396-196G-42173

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  Best Local Similarity  100.0%;  Pred. No. 3.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 CGGCGCTCGGTCAT 20
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Db         20 CGGCGCTCGGTCAT 7


RESULT 3
US-09-396-196G-46323/c
; Sequence 46323, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
;  APPLICANT: Michael Mittmann
;  APPLICANT:  David Mack
;  APPLICANT:  David Lockhart
;  APPLICANT:  Affymetrix, Inc.
;  TITLE OF INVENTION: Methods of Genetic Analysis
;  FILE REFERENCE: 3101.1
;  CURRENT APPLICATION NUMBER: US/09/396,196G
;  CURRENT FILING DATE:  1999-09-15
;  PRIOR APPLICATION NUMBER: 60/100,678
;  PRIOR FILING DATE: 1998-09-17
;  NUMBER OF SEQ ID NOS: 127806
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 46323
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: mus musculus
US-09-396-196G-46323

  Query Match            69.0%;  Score 13.8;  DB 3;  Length 25;
  Best Local Similarity  88.2%;  Pred. No. 4.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 ACGCGGCGCTCGGTCAT 20
              |||| |||| |||||||
Db         20 ACGCTGCGCACGGTCAT 4


RESULT 4
US-09-396-196G-46324/c
; Sequence 46324, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
;  APPLICANT: Michael Mittmann
;  APPLICANT:  David Mack
;  APPLICANT:  David Lockhart
;  APPLICANT:  Affymetrix, Inc.
;  TITLE OF INVENTION: Methods of Genetic Analysis
;  FILE REFERENCE: 3101.1
;  CURRENT APPLICATION NUMBER: US/09/396,196G
;  CURRENT FILING DATE:  1999-09-15
;  PRIOR APPLICATION NUMBER: 60/100,678
;  PRIOR FILING DATE: 1998-09-17
;  NUMBER OF SEQ ID NOS: 127806
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 46324
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: mus musculus
US-09-396-196G-46324

  Query Match            69.0%;  Score 13.8;  DB 3;  Length 25;
  Best Local Similarity  88.2%;  Pred. No. 4.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 ACGCGGCGCTCGGTCAT 20
              |||| |||| |||||||
Db         19 ACGCTGCGCACGGTCAT 3


RESULT 5
US-09-396-196G-46335/c
; Sequence 46335, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
;  APPLICANT: Michael Mittmann
;  APPLICANT:  David Mack
;  APPLICANT:  David Lockhart
;  APPLICANT:  Affymetrix, Inc.
;  TITLE OF INVENTION: Methods of Genetic Analysis
;  FILE REFERENCE: 3101.1
;  CURRENT APPLICATION NUMBER: US/09/396,196G
;  CURRENT FILING DATE:  1999-09-15
;  PRIOR APPLICATION NUMBER: 60/100,678
;  PRIOR FILING DATE: 1998-09-17
;  NUMBER OF SEQ ID NOS: 127806
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 46335
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: mus musculus
US-09-396-196G-46335

  Query Match            69.0%;  Score 13.8;  DB 3;  Length 25;
  Best Local Similarity  88.2%;  Pred. No. 4.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 ACGCGGCGCTCGGTCAT 20
              |||| |||| |||||||
Db         18 ACGCTGCGCACGGTCAT 2


RESULT 6
US-08-153-071-14
; Sequence 14, Application US/08153071
; Patent No. 5665869
;  GENERAL INFORMATION:
;    APPLICANT:  Ryland, James R.
;    APPLICANT:  Matthews, Maura-Ann H.
;    APPLICANT:  Ernst, Ulrich P.
;    APPLICANT:  Houk, Daniel E.
;    APPLICANT:  Traylor, David W.
;    APPLICANT:  Williams, Lee R.
;    APPLICANT:  Mitchell, David J.
;    APPLICANT:  Chivers, Mark L.
;    APPLICANT:  Belval, Thomas K.
;    TITLE OF INVENTION:  Method for the Rapid Removal of
;    TITLE OF INVENTION:  Protoporphyrin IX from Protoporphyrin IX-Containing Solutions
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Somatogen, Inc.
;      STREET:  5797 Central Avenue
;      CITY:  Boulder
;      STATE:  Colorado
;      ZIP:  80301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.4 Mb storage
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  System 7.0.1
;      SOFTWARE:  Microsoft Word 5.0a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/153,071
;      FILING DATE:  No. 5665869ember 15, 1993
;      CLASSIFICATION:  530
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;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5665869ak, Henry P.
;      REGISTRATION NUMBER:  33200
;      REFERENCE/DOCKET NUMBER:  120
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  303-541-3322
;      TELEFAX:  303-444-3013
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  42
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  primer for pBR322 ori positions
;    MOLECULE TYPE:  2380-2404
;    HYPOTHETICAL:  no
US-08-153-071-14

  Query Match             69.0%;  Score 13.8;  DB 2;  Length 42;
  Best Local Similarity   88.2%;  Pred. No. 4.4e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 ACGCGGCGCTCGGTCAT 20
              |||| |||||||||| |
Db         16 ACGCTGCGCTCGGTCGT 32


RESULT 7
US-08-609-271-21
; Sequence 21, Application US/08609271
; Patent No. 5811264
;  GENERAL INFORMATION:
;    APPLICANT:  Aitken, Jacqueline F.
;    APPLICANT:  Apostol, Izydor Z.
;    APPLICANT:  Lippincott, Julie A.
;    APPLICANT:  Levine, Joseph D.
;    TITLE OF INVENTION:  Proteins with Mutations to Decrease N-Terminal Methylatic
;    NUMBER OF SEQUENCES:  42
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Somatogen, Inc.
;      STREET:  2545 Central Avenue, Site FD-1
;      CITY:  Boulder
;      STATE:  Colorado
;      ZIP:  80301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.4 Mb storage
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  System 7.0.1
;      SOFTWARE:  Microsoft Word 5.0a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/609,271
;      FILING DATE:  28 February 1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/188,374
;      FILING DATE:  1/27/94
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5811264elli, Marianne F.
;      REGISTRATION NUMBER:  38571
;      NAME:  Brown,Theresa A.
;      REGISTRATION NUMBER:  32547
;      REFERENCE/DOCKET NUMBER:  170/Div
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  303-541-3324
;      TELEFAX:  303-444-3013
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  42
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  primer for pBR322 ori positions 2380-2404
;    HYPOTHETICAL:  no
US-08-609-271-21

  Query Match             69.0%;  Score 13.8;  DB 2;  Length 42;
  Best Local Similarity   88.2%;  Pred. No. 4.4e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 ACGCGGCGCTCGGTCAT 20
              |||| |||||||||| |
Db         16 ACGCTGCGCTCGGTCGT 32


RESULT 8
US-08-438-511-14
; Sequence 14, Application US/08438511
; Patent No. 5840851
;  GENERAL INFORMATION:
;    APPLICANT:  Plomer, J. Jeffrey
;    APPLICANT:  Ryland, James R.
;    APPLICANT:  Matthews, Maura-Ann H.
;    APPLICANT:  Traylor, David W.
;    APPLICANT:  Milne, Erin E.
;    APPLICANT:  Durfee, Steven L.
;    APPLICANT:  Mathews, Antony J.
;    APPLICANT:  Neway, Justin O.
;    TITLE OF INVENTION:  Purification of Hemoglobin
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Somatogen, Inc.
;      STREET:  2545 Central Avenue, Suite FD1
;      CITY:  Boulder
;      STATE:  Colorado
;      ZIP:  80301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.4 Mb storage
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  System 7.0.1
;      SOFTWARE:  Microsoft Word 5.0a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/438,511
;      FILING DATE:  10 May 1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/339,304
;      FILING DATE:  No. 5840851ember 14, 1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/097,273
;      FILING DATE:  July 23, 1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5840851elli, Marianne F.
;      REGISTRATION NUMBER:  38571
;      REFERENCE/DOCKET NUMBER:  191
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brown, Theresa A.
;      REGISTRATION NUMBER:  32,547
;      REFERENCE/DOCKET NUMBER:  191
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  303-541-3324
;      TELEFAX:  303-444-3013
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  42
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  primer for pBR322 ori positions 2380-2404
;    HYPOTHETICAL:  no
US-08-438-511-14

  Query Match             69.0%;  Score 13.8;  DB 2;  Length 42;
  Best Local Similarity   88.2%;  Pred. No. 4.4e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 ACGCGGCGCTCGGTCAT 20
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Db         16 ACGCTGCGCTCGGTCGT 32


RESULT 9
US-08-487-431-17
; Sequence 17, Application US/08487431
; Patent No. 5844090
;  GENERAL INFORMATION:
;    APPLICANT:  Anderson, David C.
;    APPLICANT:  Mathews, Antony J.
;    APPLICANT:  Trimble, Stephen P.
;    APPLICANT:  Anthony-Cahill, Spencer
;    TITLE OF INVENTION:  Modified Hemoglobin-like Compounds
;    NUMBER OF SEQUENCES:  30
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Somatogen, Inc.
;      STREET:  2545 Central Avenue, Suite FD1
;      CITY:  Boulder
;      STATE:  Colorado
;      ZIP:  80301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.4 Mb storage
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  System 7.5
;      SOFTWARE:  Microsoft Word 5.0a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/487,431
;      FILING DATE:  June 7, 1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/240,712
;      FILING DATE:  No. 5844090ember 6, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brown, Theresa A.
;      REGISTRATION NUMBER:  32,547
;      REFERENCE/DOCKET NUMBER:  61
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ramsey R. Stewart
;      REGISTRATION NUMBER:  38,322
;      REFERENCE/DOCKET NUMBER:  61
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  303-541-3356
;      TELEFAX:  303-444-3013
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  42
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  primer for pBR322 ori positions 2380-2404
;    HYPOTHETICAL:  no
US-08-487-431-17

  Query Match             69.0%;  Score 13.8;  DB 2;  Length 42;
  Best Local Similarity   88.2%;  Pred. No. 4.4e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 ACGCGGCGCTCGGTCAT 20
              |||| |||||||||| |
Db         16 ACGCTGCGCTCGGTCGT 32


RESULT 10
US-08-188-374-21
; Sequence 21, Application US/08188374B
; Patent No. 6140071
; GENERAL INFORMATION:
;  APPLICANT: Aitken F., Jacqueline
;  APPLICANT: Apostol, Izydor Z.
;  APPLICANT: Lippincott, Julie A.
;  APPLICANT: Levine, Joseph D.
;  TITLE OF INVENTION: Proteins with Mutations to Decrease N-Terminal Meth
;  FILE REFERENCE: BXTB 1953
;  CURRENT APPLICATION NUMBER: US/08/188,374B
;  CURRENT FILING DATE: 1994-01-27
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
;   LENGTH: 42
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: primer for
;   OTHER INFORMATION: pB32 ori positions 2380-2404
US-08-188-374-21

  Query Match             69.0%;  Score 13.8;  DB 3;  Length 42;
  Best Local Similarity   88.2%;  Pred. No. 4.4e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 ACGCGGCGCTCGGTCAT 20
              |||| |||||||||| |
Db         16 ACGCTGCGCTCGGTCGT 32


RESULT 11
US-08-973-629-17
; Sequence 17, Application US/08973629A
; Patent No. 6150506
; GENERAL INFORMATION:
;  APPLICANT: Trimble, Stephen
;  APPLICANT: Mathews, Anthony
;  APPLICANT: Kerwin, Bruce
;  APPLICANT: Marquardt, David
;  APPLICANT: Anthony-Cahill, Spencer
;  APPLICANT: Epp, Janice
;  APPLICANT: Madril, Dominic
;  APPLICANT: Anderson, David
;  TITLE OF INVENTION: MODIFIED HEMOGLOBIN-LIKE COMPOUNDS AND METHODS OF
;  TITLE OF INVENTION: PURIFYING SAME
;  FILE REFERENCE: BXTB 1928
;  CURRENT APPLICATION NUMBER: US/08/973,629A
;  CURRENT FILING DATE: 1998-08-24
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
;   LENGTH: 42
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:
;   OTHER INFORMATION: Oligonucleotide or 3' primer for generation of
;   OTHER INFORMATION: pBR332 ori with PmeI site
US-08-973-629-17

  Query Match             69.0%;  Score 13.8;  DB 3;  Length 42;
  Best Local Similarity   88.2%;  Pred. No. 4.4e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 ACGCGGCGCTCGGTCAT 20
              |||| |||||||||| |
Db         16 ACGCTGCGCTCGGTCGT 32


RESULT 12
US-09-396-196G-53301
; Sequence 53301, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
;  APPLICANT: Michael Mittmann
;  APPLICANT:  David Mack
;  APPLICANT:  David Lockhart
;  APPLICANT:  Affymetrix, Inc.
;  TITLE OF INVENTION: Methods of Genetic Analysis
;  FILE REFERENCE: 3101.1
```

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;  CURRENT APPLICATION NUMBER: US/09/396,196G
;  CURRENT FILING DATE:  1999-09-15
;  PRIOR APPLICATION NUMBER: 60/100,678
;  PRIOR FILING DATE: 1998-09-17
;  NUMBER OF SEQ ID NOS: 127806
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 53301
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: mus musculus
US-09-396-196G-53301

  Query Match             66.0%;  Score 13.2;  DB 3;  Length 25;
  Best Local Similarity   83.3%;  Pred. No. 8.3e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 GACGCGGCGCTCGGTCAT 20
              ||| | ||||||  |||||
Db          2 GACCCAGCGCTCTGTCAT 19


RESULT 13
US-09-046-858A-19
; Sequence 19, Application US/09046858A
; Patent No. 6048973
;  GENERAL INFORMATION:
;    APPLICANT:  Rodriguez, Raymond L.
;    TITLE OF INVENTION:  SUGAR-REGULATORY SEQUENCES
;    TITLE OF INVENTION:  IN ALPHA-AMYLASE GENES
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dehlinger & Associates
;      STREET:  PO Box 60850
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/046,858A
;      FILING DATE:  24-MAR-1998
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/042,376
;      FILING DATE:  24-MAR-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dehlinger, Peter J.
;      REGISTRATION NUMBER:  28,006
;      REFERENCE/DOCKET NUMBER:  2000-0456.30
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-324-0880
;      TELEFAX:  650-324-0960
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-046-858A-19

  Query Match             65.0%;  Score 13;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1e+04;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 GACGCGGCGCTCG 15
              |||||||||||||
Db          2 GACGCGGCGCTCG 14


RESULT 14
US-09-450-515-19
; Sequence 19, Application US/09450515
; Patent No. 6680425
;  GENERAL INFORMATION:
;       APPLICANT: Rodriguez, Raymond L.
;       TITLE OF INVENTION: SUGAR-REGULATORY SEQUENCES
;                           IN ALPHA-AMYLASE GENES
;       NUMBER OF SEQUENCES: 21
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Dehlinger & Associates
;            STREET: PO Box 60850
;            CITY: Palo Alto
;            STATE: CA
;            COUNTRY: USA
;            ZIP: 94306
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: DOS
;            SOFTWARE: FastSEQ for Windows Version 2.0
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/450,515
;            FILING DATE: 29-No. 6680425-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/046,858
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Dehlinger, Peter J.
;            REGISTRATION NUMBER: 28,006
;            REFERENCE/DOCKET NUMBER: 2000-0456.30
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 650-324-0880
;            TELEFAX: 650-324-0960
;            TELEX: <Unknown>
;  INFORMATION FOR SEQ ID NO: 19:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 20 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-450-515-19

  Query Match             65.0%;  Score 13;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1e+04;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 GACGCGGCGCTCG 15
              |||||||||||||
Db          2 GACGCGGCGCTCG 14


RESULT 15
US-10-206-654-19
; Sequence 19, Application US/10206654
; Patent No. 6919493
;  GENERAL INFORMATION:
;       APPLICANT: Rodriguez, Raymond L.
;       TITLE OF INVENTION: SUGAR-REGULATORY SEQUENCES
;                           IN ALPHA-AMYLASE GENES
;       NUMBER OF SEQUENCES: 21
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Dehlinger & Associates
;            STREET: PO Box 60850
;            CITY: Palo Alto
;            STATE: CA
;            COUNTRY: USA
;            ZIP: 94306
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette
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;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: FastSEQ for Windows Version 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/206,654
;             FILING DATE: 25-Jul-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/046,858A
;             FILING DATE: 24-MAR-1998
;             APPLICATION NUMBER: 60/042,376
;             FILING DATE: 24-MAR-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Dehlinger, Peter J.
;             REGISTRATION NUMBER: 28,006
;             REFERENCE/DOCKET NUMBER: 2000-0456.30
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 650-324-0880
;             TELEFAX: 650-324-0960
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 19:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 20 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-206-654-19

  Query Match             65.0%;  Score 13;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1e+04;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 GACGCGGCGCTCG 15
              |||||||||||||
Db          2 GACGCGGCGCTCG 14


Search completed: December 13, 2005, 14:32:05
Job time : 95 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 13:25:43 ; Search time 445 Seconds
(without alignments)
371.657 Million cell updates/sec

Title: US-10-605-498-82
Perfect score: 20
Sequence: 1 gggacgcggcgctcggtcat 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 11091250

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_Main:*
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2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
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5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	20	100.0	20	7	US-10-605-498-82	Sequence 82, Appl
	2	20	100.0	21	7	US-10-605-498-81	Sequence 81, Appl
c	3	19	95.0	19	7	US-10-605-498-90	Sequence 90, Appl
	4	16	80.0	21	7	US-10-605-498-3	Sequence 3, Appli
c	5	15.2	76.0	25	7	US-10-719-956-135321	Sequence 135321,
	6	15	75.0	21	7	US-10-605-498-4	Sequence 4, Appli
	7	14.2	71.0	25	10	US-11-036-317-261850	Sequence 261850,
	8	14.2	71.0	25	10	US-11-036-317-269817	Sequence 269817,
	9	14.2	71.0	25	10	US-11-036-317-330516	Sequence 330516,
	10	14.2	71.0	25	10	US-11-036-317-332488	Sequence 332488,
	11	14.2	71.0	25	10	US-11-036-317-364465	Sequence 364465,
	12	14.2	71.0	25	10	US-11-036-317-406575	Sequence 406575,
	13	14.2	71.0	25	10	US-11-036-317-536426	Sequence 536426,
	14	14.2	71.0	25	10	US-11-036-317-536427	Sequence 536427,
	15	14.2	71.0	33	3	US-09-977-137A-16	Sequence 16, Appl
	16	14	70.0	25	5	US-10-215-112-7242	Sequence 7242, Ap
c	17	14	70.0	25	9	US-10-809-189-42173	Sequence 42173, A
c	18	13.8	69.0	25	9	US-10-809-189-46323	Sequence 46323, A
c	19	13.8	69.0	25	9	US-10-809-189-46324	Sequence 46324, A
c	20	13.8	69.0	25	9	US-10-809-189-46335	Sequence 46335, A
c	21	13.6	68.0	25	7	US-10-719-956-135322	Sequence 135322,
	22	13.6	68.0	25	7	US-10-719-956-198103	Sequence 198103,
	23	13.6	68.0	25	8	US-10-719-900-309243	Sequence 309243,
	24	13.6	68.0	25	10	US-11-036-317-912027	Sequence 912027,
	25	13.6	68.0	25	10	US-11-036-317-912041	Sequence 912041,
c	26	13.2	66.0	25	5	US-10-098-263B-3853	Sequence 3853, Ap
	27	13.2	66.0	25	5	US-10-098-263B-65789	Sequence 65789, A
	28	13.2	66.0	25	7	US-10-719-956-110491	Sequence 110491,
c	29	13.2	66.0	25	7	US-10-719-956-547822	Sequence 547822,
c	30	13.2	66.0	25	7	US-10-719-956-547823	Sequence 547823,
	31	13.2	66.0	25	8	US-10-719-900-148603	Sequence 148603,
	32	13.2	66.0	25	8	US-10-719-900-849503	Sequence 849503,
	33	13.2	66.0	25	8	US-10-719-900-849504	Sequence 849504,
	34	13.2	66.0	25	9	US-10-809-189-53301	Sequence 53301, A
	35	13.2	66.0	25	10	US-11-036-317-321539	Sequence 321539,
	36	13.2	66.0	25	10	US-11-036-317-787134	Sequence 787134,
c	37	13.2	66.0	25	10	US-11-060-756-166335	Sequence 166335,
c	38	13.2	66.0	25	10	US-11-060-756-166384	Sequence 166384,
c	39	13.2	66.0	25	10	US-11-060-756-229339	Sequence 229339,
c	40	13.2	66.0	25	10	US-11-060-756-229340	Sequence 229340,
	41	13.2	66.0	43	3	US-09-792-630-48	Sequence 48, Appl
	42	13.2	66.0	43	3	US-09-953-351-48	Sequence 48, Appl
	43	13.2	66.0	43	5	US-10-080-376-48	Sequence 48, Appl
	44	13.2	66.0	43	5	US-10-082-671-54	Sequence 54, Appl
	45	13.2	66.0	43	5	US-10-097-100-48	Sequence 48, Appl

ALIGNMENTS

RESULT 1
US-10-605-498-82
; Sequence 82, Application US/10605498
; Publication No. US20040127441A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rocchi, Palma
; APPLICANT: Signaevsky, Maxim
; TITLE OF INVENTION: Compositions and Methods for Treatment of Prostate and Other
; TITLE OF INVENTION: Cancers
; FILE REFERENCE: UBC.P-031
; CURRENT APPLICATION NUMBER: US/10/605,498
; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,859
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/463,952
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 82
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-605-498-82

Query Match 100.0%; Score 20; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GGGACGCGGCGCTCGGTCAT 20
              ||||||||||||||||||||
Db          1 GGGACGCGGCGCTCGGTCAT 20
```

RESULT 2
US-10-605-498-81
; Sequence 81, Application US/10605498
; Publication No. US20040127441A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rocchi, Palma
; APPLICANT: Signaevsky, Maxim
; TITLE OF INVENTION: Compositions and Methods for Treatment of Prostate and Other
; TITLE OF INVENTION: Cancers
; FILE REFERENCE: UBC.P-031
; CURRENT APPLICATION NUMBER: US/10/605,498

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;  CURRENT FILING DATE:  2003-10-02
;  PRIOR APPLICATION NUMBER: US 60/415,859
;  PRIOR FILING DATE: 2002-10-02
;  PRIOR APPLICATION NUMBER: US 60/463,952
;  PRIOR FILING DATE: 2003-04-18
;  NUMBER OF SEQ ID NOS: 91
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 81
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-605-498-81

  Query Match            100.0%;  Score 20;  DB 7;  Length 21;
  Best Local Similarity  100.0%;  Pred. No. 5.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGGACGCGGCGCTCGGTCAT 20
              ||||||||||||||||||||
Db          2 GGGACGCGGCGCTCGGTCAT 21


RESULT 3
US-10-605-498-90/c
; Sequence 90, Application US/10605498
; Publication No. US20040127441A1
; GENERAL INFORMATION:
;  APPLICANT: Gleave, Martin
;  APPLICANT:  Rocchi, Palma
;  APPLICANT:  Signaevsky, Maxim
;  TITLE OF INVENTION: Compositions and Methods for Treatment of Prostate and Other
;  TITLE OF INVENTION:  Cancers
;  FILE REFERENCE: UBC.P-031
;  CURRENT APPLICATION NUMBER: US/10/605,498
;  CURRENT FILING DATE:  2003-10-02
;  PRIOR APPLICATION NUMBER: US 60/415,859
;  PRIOR FILING DATE: 2002-10-02
;  PRIOR APPLICATION NUMBER: US 60/463,952
;  PRIOR FILING DATE: 2003-04-18
;  NUMBER OF SEQ ID NOS: 91
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 90
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-605-498-90

  Query Match            95.0%;  Score 19;  DB 7;  Length 19;
  Best Local Similarity  100.0%;  Pred. No. 17;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GGACGCGGCGCTCGGTCAT 20
              ||||||||||||||||||
Db         19 GGACGCGGCGCTCGGTCAT 1


RESULT 4
US-10-605-498-3
; Sequence 3, Application US/10605498
; Publication No. US20040127441A1
; GENERAL INFORMATION:
;  APPLICANT: Gleave, Martin
;  APPLICANT:  Rocchi, Palma
;  APPLICANT:  Signaevsky, Maxim
;  TITLE OF INVENTION: Compositions and Methods for Treatment of Prostate and Other
;  TITLE OF INVENTION:  Cancers
;  FILE REFERENCE: UBC.P-031
;  CURRENT APPLICATION NUMBER: US/10/605,498
;  CURRENT FILING DATE:  2003-10-02
;  PRIOR APPLICATION NUMBER: US 60/415,859
;  PRIOR FILING DATE: 2002-10-02
;  PRIOR APPLICATION NUMBER: US 60/463,952
;  PRIOR FILING DATE: 2003-04-18
;  NUMBER OF SEQ ID NOS: 91
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-605-498-3

  Query Match            80.0%;  Score 16;  DB 7;  Length 21;
  Best Local Similarity  100.0%;  Pred. No. 4.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CGCGGCGCTCGGTCAT 20
              ||||||||||||||||
Db          1 CGCGGCGCTCGGTCAT 16


RESULT 5
US-10-719-956-135321/c
; Sequence 135321, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
;  APPLICANT: Xue Mei Zhou
;  TITLE OF INVENTION: Methods of Genetic Analysis of Rat
;  FILE REFERENCE: 3527.1
;  CURRENT APPLICATION NUMBER: US/10/719,956
;  CURRENT FILING DATE:  2003-11-20
;  PRIOR APPLICATION NUMBER: 60/427,836
;  PRIOR FILING DATE: 2002 11 20
;  NUMBER OF SEQ ID NOS: 699466
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 135321
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
US-10-719-956-135321

  Query Match            76.0%;  Score 15.2;  DB 7;  Length 25;
  Best Local Similarity  85.0%;  Pred. No. 1.2e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GGGACGCGGCGCTCGGTCAT 20
              |||||||  ||||||| |||
Db         25 GGGACGCAACGCTCGGCCAT 6


RESULT 6
US-10-605-498-4
; Sequence 4, Application US/10605498
; Publication No. US20040127441A1
; GENERAL INFORMATION:
;  APPLICANT: Gleave, Martin
;  APPLICANT:  Rocchi, Palma
;  APPLICANT:  Signaevsky, Maxim
;  TITLE OF INVENTION: Compositions and Methods for Treatment of Prostate and Other
;  TITLE OF INVENTION:  Cancers
;  FILE REFERENCE: UBC.P-031
;  CURRENT APPLICATION NUMBER: US/10/605,498
;  CURRENT FILING DATE:  2003-10-02
;  PRIOR APPLICATION NUMBER: US 60/415,859
;  PRIOR FILING DATE: 2002-10-02
;  PRIOR APPLICATION NUMBER: US 60/463,952
;  PRIOR FILING DATE: 2003-04-18
;  NUMBER OF SEQ ID NOS: 91
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-605-498-4

  Query Match            75.0%;  Score 15;  DB 7;  Length 21;
  Best Local Similarity  100.0%;  Pred. No. 1.5e+03;
```

```
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGGACGCGGCGCTCG 15
              ||||||||||||||||
Db          7 GGGACGCGGCGCTCG 21


RESULT 7
US-11-036-317-261850
; Sequence 261850, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
;  APPLICANT: Williams, Alan
;  APPLICANT:  Blume, John
;  TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
;  FILE REFERENCE: 3654.1
;  CURRENT APPLICATION NUMBER: US/11/036,317
;  CURRENT FILING DATE:  2005-01-13
;  PRIOR APPLICATION NUMBER: US 60/536,639
;  PRIOR FILING DATE: 2004-01-13
;  NUMBER OF SEQ ID NOS: 991174
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 261850
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-11-036-317-261850

  Query Match             71.0%;  Score 14.2;  DB 10;  Length 25;
  Best Local Similarity   84.2%;  Pred. No. 3.6e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GGGACGCGGCGCTCGGTCA 19
              ||||||||||| || | ||
Db          3 GGGACGCGGCGATCTGCCA 21


RESULT 8
US-11-036-317-269817
; Sequence 269817, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
;  APPLICANT: Williams, Alan
;  APPLICANT:  Blume, John
;  TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
;  FILE REFERENCE: 3654.1
;  CURRENT APPLICATION NUMBER: US/11/036,317
;  CURRENT FILING DATE:  2005-01-13
;  PRIOR APPLICATION NUMBER: US 60/536,639
;  PRIOR FILING DATE: 2004-01-13
;  NUMBER OF SEQ ID NOS: 991174
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 269817
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-11-036-317-269817

  Query Match             71.0%;  Score 14.2;  DB 10;  Length 25;
  Best Local Similarity   84.2%;  Pred. No. 3.6e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GGGACGCGGCGCTCGGTCA 19
              ||||||||||| || | ||
Db          5 GGGACGCGGCGATCTGCCA 23


RESULT 9
US-11-036-317-330516
; Sequence 330516, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
;  APPLICANT: Williams, Alan
;  APPLICANT:  Blume, John
;  TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
;  FILE REFERENCE: 3654.1
;  CURRENT APPLICATION NUMBER: US/11/036,317
;  CURRENT FILING DATE:  2005-01-13
;  PRIOR APPLICATION NUMBER: US 60/536,639
;  PRIOR FILING DATE: 2004-01-13
;  NUMBER OF SEQ ID NOS: 991174
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 330516
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-11-036-317-330516

  Query Match             71.0%;  Score 14.2;  DB 10;  Length 25;
  Best Local Similarity   84.2%;  Pred. No. 3.6e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GGGACGCGGCGCTCGGTCA 19
              ||||||||||| || | ||
Db          1 GGGACGCGGCGATCTGCCA 19


RESULT 10
US-11-036-317-332488
; Sequence 332488, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
;  APPLICANT: Williams, Alan
;  APPLICANT:  Blume, John
;  TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
;  FILE REFERENCE: 3654.1
;  CURRENT APPLICATION NUMBER: US/11/036,317
;  CURRENT FILING DATE:  2005-01-13
;  PRIOR APPLICATION NUMBER: US 60/536,639
;  PRIOR FILING DATE: 2004-01-13
;  NUMBER OF SEQ ID NOS: 991174
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 332488
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-11-036-317-332488

  Query Match             71.0%;  Score 14.2;  DB 10;  Length 25;
  Best Local Similarity   84.2%;  Pred. No. 3.6e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GGGACGCGGCGCTCGGTCA 19
              ||||||||||| || | ||
Db          2 GGGACGCGGCGATCTGCCA 20


RESULT 11
US-11-036-317-364465
; Sequence 364465, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
;  APPLICANT: Williams, Alan
;  APPLICANT:  Blume, John
;  TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
;  FILE REFERENCE: 3654.1
;  CURRENT APPLICATION NUMBER: US/11/036,317
;  CURRENT FILING DATE:  2005-01-13
;  PRIOR APPLICATION NUMBER: US 60/536,639
;  PRIOR FILING DATE: 2004-01-13
;  NUMBER OF SEQ ID NOS: 991174
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 364465
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
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US-11-036-317-364465

Query Match 71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 3.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGACGCGGCGCTCGGTCA 19
||||||||||| || | ||
Db 4 GGGACGCGGCGATCTGCCA 22

RESULT 12
US-11-036-317-406575
; Sequence 406575, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 406575
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-406575

Query Match 71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 3.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGACGCGGCGCTCGGTCA 19
|||||| |||||| ||||
Db 7 GGGACGAGGCGCTTTGTCA 25

RESULT 13
US-11-036-317-536426
; Sequence 536426, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 536426
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-536426

Query Match 71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 3.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGACGCGGCGCTCGGTCA 19
|||||| |||||| ||||
Db 7 GGGACGAGGCGCTTTGTCA 25

RESULT 14
US-11-036-317-536427
; Sequence 536427, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 536427
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-536427

Query Match 71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 3.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGACGCGGCGCTCGGTCA 19
|||||| |||||| ||||
Db 7 GGGACGTGGCGCTTTGTCA 25

RESULT 15
US-09-977-137A-16
; Sequence 16, Application US/09977137A
; Publication No. US20030104524A1
; GENERAL INFORMATION:
; APPLICANT: Summers, Anne O.
; APPLICANT: Caguiat, Jonathan
; TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 79-00
; CURRENT APPLICATION NUMBER: US/09/977,137A
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/240,465
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-977-137A-16

Query Match 71.0%; Score 14.2; DB 3; Length 33;
Best Local Similarity 84.2%; Pred. No. 3.4e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGACGCGGCGCTCGGTCA 19
||| | |||||||||| ||
Db 6 GGGTCTCGGCGCTCGGGCA 24

Search completed: December 13, 2005, 14:39:40
Job time : 446 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 13:30:05 ; Search time 144 Seconds
(without alignments)
51.924 Million cell updates/sec

Title: US-10-605-498-82
Perfect score: 20
Sequence: 1 gggacgcggcgctcggtcat 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3392430 seqs, 186927314 residues

Total number of hits satisfying chosen parameters: 6638722

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*
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3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
10: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	12.8	64.0	19	8	US-11-101-244-1008030	Sequence 1008030,
c	2	12.8	64.0	19	9	US-11-083-784-1008030	Sequence 1008030,
	3	12.6	63.0	19	8	US-11-101-244-899787	Sequence 899787,
	4	12.6	63.0	19	9	US-11-083-784-899787	Sequence 899787,
c	5	12.4	62.0	32	6	US-10-939-294A-16099	Sequence 16099, A
c	6	12.2	61.0	22	7	US-11-176-795-58	Sequence 58, Appl
c	7	12.2	61.0	22	7	US-11-176-795-62	Sequence 62, Appl
	8	12.2	61.0	32	6	US-10-939-294A-15630	Sequence 15630, A
c	9	12	60.0	19	8	US-11-101-244-877585	Sequence 877585,
c	10	12	60.0	19	9	US-11-083-784-877585	Sequence 877585,
c	11	12	60.0	27	7	US-11-075-046-4	Sequence 4, Appli
c	12	12	60.0	32	7	US-11-075-046-30	Sequence 30, Appl
c	13	11.8	59.0	19	8	US-11-101-244-367704	Sequence 367704,
c	14	11.8	59.0	19	8	US-11-101-244-367714	Sequence 367714,
c	15	11.8	59.0	19	8	US-11-101-244-385820	Sequence 385820,
	16	11.8	59.0	19	8	US-11-101-244-475963	Sequence 475963,
c	17	11.8	59.0	19	8	US-11-101-244-1128971	Sequence 1128971,
c	18	11.8	59.0	19	8	US-11-101-244-1221629	Sequence 1221629,
c	19	11.8	59.0	19	9	US-11-083-784-367704	Sequence 367704,
c	20	11.8	59.0	19	9	US-11-083-784-367714	Sequence 367714,
c	21	11.8	59.0	19	9	US-11-083-784-385820	Sequence 385820,
	22	11.8	59.0	19	9	US-11-083-784-475963	Sequence 475963,
c	23	11.8	59.0	19	9	US-11-083-784-1128971	Sequence 1128971,
c	24	11.8	59.0	19	9	US-11-083-784-1221629	Sequence 1221629,
	25	11.6	58.0	18	6	US-10-231-302-31	Sequence 31, Appl
	26	11.6	58.0	19	8	US-11-101-244-992967	Sequence 992967,
	27	11.6	58.0	19	8	US-11-101-244-1512341	Sequence 1512341,
	28	11.6	58.0	19	8	US-11-101-244-1562938	Sequence 1562938,
	29	11.6	58.0	19	9	US-11-083-784-992967	Sequence 992967,
	30	11.6	58.0	19	9	US-11-083-784-1512341	Sequence 1512341,
	31	11.6	58.0	19	9	US-11-083-784-1562938	Sequence 1562938,
	32	11.6	58.0	20	7	US-11-069-908-929	Sequence 929, App
	33	11.6	58.0	20	7	US-11-069-908-3295	Sequence 3295, Ap
	34	11.6	58.0	32	6	US-10-939-294A-15939	Sequence 15939, A
c	35	11.6	58.0	32	6	US-10-939-294A-16630	Sequence 16630, A
c	36	11.6	58.0	32	6	US-10-939-294A-17166	Sequence 17166, A
	37	11.6	58.0	32	6	US-10-939-294A-18354	Sequence 18354, A
	38	11.6	58.0	32	6	US-10-939-294A-18436	Sequence 18436, A
c	39	11.6	58.0	35	6	US-10-525-710-67	Sequence 67, Appl
	40	11.4	57.0	19	8	US-11-101-244-199478	Sequence 199478,
	41	11.4	57.0	19	8	US-11-101-244-199517	Sequence 199517,
c	42	11.4	57.0	19	8	US-11-101-244-386259	Sequence 386259,
c	43	11.4	57.0	19	8	US-11-101-244-1044567	Sequence 1044567,
	44	11.4	57.0	19	8	US-11-101-244-1436226	Sequence 1436226,
	45	11.4	57.0	19	9	US-11-083-784-199478	Sequence 199478,

ALIGNMENTS

RESULT 1
US-11-101-244-1008030/c
; Sequence 1008030, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1008030
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1008030

Query Match 64.0%; Score 12.8; DB 8; Length 19;
Best Local Similarity 87.5%; Pred. No. 3.4e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          3 GACGCGGCGCTCGGTC 18
              || | ||||||||||||
Db         17 GATGAGGCGCTCGGTC 2
```

RESULT 2
US-11-083-784-1008030/c
; Sequence 1008030, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William

```
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/083,784
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US/10/714,333
;  PRIOR FILING DATE: 2003-11-14
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 1008030
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-083-784-1008030

  Query Match             64.0%;  Score 12.8;  DB 9;  Length 19;
  Best Local Similarity   87.5%;  Pred. No. 3.4e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3 GACGCGGCGCTCGGTC 18
           || | ||||||||||
Db      17 GATGAGGCGCTCGGTC 2
```

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RESULT 3
US-11-101-244-899787
; Sequence 899787, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/101,244
;  CURRENT FILING DATE:  2005-04-07
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 899787
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-101-244-899787

  Query Match             63.0%;  Score 12.6;  DB 8;  Length 19;
  Best Local Similarity   63.2%;  Pred. No. 4.2e+03;
  Matches   12;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 GGACGCGGCGCTCGGTCAT 20
              |||  ||||||: | :||:
Db          1 GGAAACGGCGCUGGUUCAU 19
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RESULT 4
US-11-083-784-899787
; Sequence 899787, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/083,784
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US/10/714,333
;  PRIOR FILING DATE: 2003-11-14
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 899787
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-083-784-899787

  Query Match             63.0%;  Score 12.6;  DB 9;  Length 19;
  Best Local Similarity   63.2%;  Pred. No. 4.2e+03;
  Matches   12;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 GGACGCGGCGCTCGGTCAT 20
              |||  ||||||: | :||:
Db          1 GGAAACGGCGCUGGUUCAU 19
```

```
RESULT 5
US-10-939-294A-16099/c
; Sequence 16099, Application US/10939294A
; Publication No. US20050266417A1
; GENERAL INFORMATION:
;  APPLICANT: Barany, Francis
;  APPLICANT:  Turner, Daniel
;  APPLICANT:  Pingle, Maneesh
;  APPLICANT:  Pincas, Hanna
;  TITLE OF INVENTION: Methods for identifying target nucleic acid molecules
;  FILE REFERENCE: 19603/4121 (CRF D-2995-02)
;  CURRENT APPLICATION NUMBER: US/10/939,294A
;  CURRENT FILING DATE:  2004-09-10
;  PRIOR APPLICATION NUMBER: US 60/502/731
;  PRIOR FILING DATE: 2003-09-12
;  NUMBER OF SEQ ID NOS: 38895
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16099
;   LENGTH: 32
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: oligonucleotide probe
US-10-939-294A-16099

  Query Match             62.0%;  Score 12.4;  DB 6;  Length 32;
  Best Local Similarity   92.9%;  Pred. No. 4.7e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGGACGCGGCGCTC 14
              |||||||| |||||
Db         21 GGGACGCGTCGCTC 8
```

```
RESULT 6
US-11-176-795-58/c
; Sequence 58, Application US/11176795
; Publication No. US20050255517A1
; GENERAL INFORMATION:
;  APPLICANT: Gerdes, John C
;  APPLICANT:  Marmaro, Jeffrey M
;  TITLE OF INVENTION: Method and Device for Multiplex Amplification System
;  FILE REFERENCE: 1
;  CURRENT APPLICATION NUMBER: US/11/176,795
```

```
;  CURRENT FILING DATE:  2005-07-07
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 58
;    LENGTH: 22
;    TYPE: DNA
;    ORGANISM: Coliform Bacteria
US-11-176-795-58

  Query Match             61.0%;  Score 12.2;  DB 7;  Length 22;
  Best Local Similarity   82.4%;  Pred. No. 6e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 GGACGCGGCGCTCGGTC 18
              ||| ||||||  |||||
Db         19 GGATGCGGCGTGCGGTC 3


RESULT 7
US-11-176-795-62/c
; Sequence 62, Application US/11176795
; Publication No. US20050255517A1
; GENERAL INFORMATION:
;  APPLICANT: Gerdes, John C
;  APPLICANT:  Marmaro, Jeffrey M
;  TITLE OF INVENTION: Method and Device for Multiplex Amplification System
;  FILE REFERENCE: 1
;  CURRENT APPLICATION NUMBER: US/11/176,795
;  CURRENT FILING DATE:  2005-07-07
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
;    LENGTH: 22
;    TYPE: DNA
;    ORGANISM: Coliform Bacteria
US-11-176-795-62

  Query Match             61.0%;  Score 12.2;  DB 7;  Length 22;
  Best Local Similarity   82.4%;  Pred. No. 6e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 GGACGCGGCGCTCGGTC 18
              ||| ||||||  |||||
Db         19 GGATGCGGCGTGCGGTC 3


RESULT 8
US-10-939-294A-15630
; Sequence 15630, Application US/10939294A
; Publication No. US20050266417A1
; GENERAL INFORMATION:
;  APPLICANT: Barany, Francis
;  APPLICANT:  Turner, Daniel
;  APPLICANT:  Pingle, Maneesh
;  APPLICANT:  Pincas, Hanna
;  TITLE OF INVENTION: Methods for identifying target nucleic acid molecules
;  FILE REFERENCE: 19603/4121 (CRF D-2995-02)
;  CURRENT APPLICATION NUMBER: US/10/939,294A
;  CURRENT FILING DATE:  2004-09-10
;  PRIOR APPLICATION NUMBER: US 60/502/731
;  PRIOR FILING DATE: 2003-09-12
;  NUMBER OF SEQ ID NOS: 38895
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15630
;    LENGTH: 32
;    TYPE: DNA
;    ORGANISM: Artificial
;    FEATURE:
;    OTHER INFORMATION: oligonucleotide probe
US-10-939-294A-15630

  Query Match             61.0%;  Score 12.2;  DB 6;  Length 32;
  Best Local Similarity   82.4%;  Pred. No. 5.7e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 GGACGCGGCGCTCGGTC 18
              ||| ||||||  |||||
Db          8 GGACGCGGAACGCGGTC 24


RESULT 9
US-11-101-244-877585/c
; Sequence 877585, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/101,244
;  CURRENT FILING DATE:  2005-04-07
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 877585
;    LENGTH: 19
;    TYPE: RNA
;    ORGANISM: Homo sapiens
US-11-101-244-877585

  Query Match             60.0%;  Score 12;  DB 8;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 7.5e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 GCGCTCGGTCAT 20
              ||||||||||||
Db         15 GCGCTCGGTCAT 4


RESULT 10
US-11-083-784-877585/c
; Sequence 877585, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/083,784
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US/10/714,333
;  PRIOR FILING DATE: 2003-11-14
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 877585
;    LENGTH: 19
;    TYPE: RNA
;    ORGANISM: Homo sapiens
US-11-083-784-877585

  Query Match             60.0%;  Score 12;  DB 9;  Length 19;
```

```
  Best Local Similarity   100.0%;  Pred. No. 7.5e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 GCGCTCGGTCAT 20
              ||||||||||||
Db         15 GCGCTCGGTCAT 4


RESULT 11
US-11-075-046-4/c
; Sequence 4, Application US/11075046
; Publication No. US20050268353A1
;  GENERAL INFORMATION:
;    APPLICANT:  P. D. CHRISTIAN, K. H. J. GORDON and
;    APPLICANT:  T. N. HANZLIK
;    TITLE OF INVENTION:  INSECT VIRUSES AND THEIR USES IN
;    TITLE OF INVENTION:  PROTECTING PLANTS
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DORSEY & WHITNEY LLP
;      STREET:  FOUR EMBARCADERO CENTER, SUITE 3400
;      CITY:  SAN FRANCISCO
;      STATE:  CALIFORNIA
;      COUNTRY:  UNITED STATES OF AMERICA
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/11/075,046
;      FILING DATE:  07-MAR-2005
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/677,653
;      FILING DATE:  03-Oct-2000
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  RICHARD F. TRECARTIN
;      REGISTRATION NUMBER:  31,801
;      REFERENCE/DOCKET NUMBER:  A-58631-4/RFT/NBC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 781-1989
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  27 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-11-075-046-4

  Query Match             60.0%;  Score 12;  DB 7;  Length 27;
  Best Local Similarity   75.0%;  Pred. No. 7.1e+03;
  Matches   15;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GGGACGCGGCGCTCGGTCAT 20
              | |||||  |  |||| ||||
Db         20 GCGACGCCGGCCTCGCTCAT 1


RESULT 12
US-11-075-046-30/c
; Sequence 30, Application US/11075046
; Publication No. US20050268353A1
;  GENERAL INFORMATION:
;    APPLICANT:  P. D. CHRISTIAN, K. H. J. GORDON and
;    APPLICANT:  T. N. HANZLIK
;    TITLE OF INVENTION:  INSECT VIRUSES AND THEIR USES IN
;    TITLE OF INVENTION:  PROTECTING PLANTS
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DORSEY & WHITNEY LLP
;      STREET:  FOUR EMBARCADERO CENTER, SUITE 3400
;      CITY:  SAN FRANCISCO
;      STATE:  CALIFORNIA
;      COUNTRY:  UNITED STATES OF AMERICA
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/11/075,046
;      FILING DATE:  07-MAR-2005
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/677,653
;      FILING DATE:  03-Oct-2000
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  RICHARD F. TRECARTIN
;      REGISTRATION NUMBER:  31,801
;      REFERENCE/DOCKET NUMBER:  A-58631-4/RFT/NBC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 781-1989
;  INFORMATION FOR SEQ ID NO:  30:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  32 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  6..32
US-11-075-046-30

  Query Match             60.0%;  Score 12;  DB 7;  Length 32;
  Best Local Similarity   75.0%;  Pred. No. 6.9e+03;
  Matches   15;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GGGACGCGGCGCTCGGTCAT 20
              | |||||  |  |||| ||||
Db         25 GCGACGCCGGCCTCGCTCAT 6


RESULT 13
US-11-101-244-367704/c
; Sequence 367704, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/101,244
;  CURRENT FILING DATE:  2005-04-07
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 367704
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-101-244-367704

  Query Match             59.0%;  Score 11.8;  DB 8;  Length 19;
  Best Local Similarity   86.7%;  Pred. No. 9.1e+03;
```

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          4 ACGCGGCGCTCGGTC 18
              || ||||||| ||||
Db         16 ACACGGCGCTTGGTC 2
```

RESULT 14
US-11-101-244-367714/c
; Sequence 367714, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 367714
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-367714

Query Match 59.0%; Score 11.8; DB 8; Length 19;
Best Local Similarity 86.7%; Pred. No. 9.1e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          4 ACGCGGCGCTCGGTC 18
              || ||||||| ||||
Db         15 ACACGGCGCTTGGTC 1
```

RESULT 15
US-11-101-244-385820/c
; Sequence 385820, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 385820
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-385820

Query Match 59.0%; Score 11.8; DB 8; Length 19;
Best Local Similarity 86.7%; Pred. No. 9.1e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          3 GACGCGGCGCTCGGT 17
              || | ||||||||||
Db         17 GAGGTGGCGCTCGGT 3
```

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Job time : 144 secs